

Sequence Listing

<110> Ashkenazi, Avi
 Baker Kevin P.
 Botstein, David
 Desnoyers, Luc
 Eaton, Dan
 Ferrara, Napoleon
 Filvaroff, Ellen
 Fong, Sherman
 Gao, Wei-Qiang
 Gerber, Hanspeter
 Gerritsen, Mary E.
 Goddard, Audrey
 Godowski, Paul J.
 Grimaldi, J. Christopher
 Gurney, Austin L.
 Hillan, Kenneth J
 Kljavin, Ivar J.
 Kuo, Sophia S.
 Napier, Mary A.
 Pan, James;
 Paoni, Nicholas F.
 Roy, Margaret Ann
 Shelton, David L.
 Stewart, Timothy A.
 Tumas, Daniel
 Williams, P. Mickey
 Wood, William I.

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Asp Glu Ser Val Gly Ser Lys Thr Arg Arg Ala Phe Leu Tyr Leu	125		130		135
Ala Ala Phe Pro Phe Met Asp Ala Met Ala Trp Thr His Ala Gly	140		145		150
Ile Leu Leu Lys His Lys Tyr Ser Phe Leu Val Gly Cys Ala Ser	155		160		165
Ile Ser Asp Val Ile Ala Gln Val Val Phe Val Ala Ile Leu Leu	170		175		180
His Ser His Leu Glu Cys Arg Glu Pro Leu Leu Ile Pro Ile Leu	185		190		195
Ser Leu Tyr Met Gly Ala Leu Val Arg Cys Thr Thr Leu Cys Leu	200		205		210
Gly Tyr Tyr Lys Asn Ile His Asp Ile Ile Pro Asp Arg Ser Gly	215		220		225
Pro Glu Leu Gly Gly Asp Ala Thr Ile Arg Lys Met Leu Ser Phe	230		235		240
Trp Trp Pro Leu Ala Leu Ile Leu Ala Thr Gln Arg Ile Ser Arg	245		250		255
Pro Ile Val Asn Leu Phe Val Ser Arg Asp Leu Gly Gly Ser Ser	260		265		270
Ala Ala Thr Glu Ala Val Ala Ile Leu Thr Ala Thr Tyr Pro Val	275		280		285
Gly His Met Pro Tyr Gly Trp Leu Thr Glu Ile Arg Ala Val Tyr	290		295		300
Pro Ala Phe Asp Lys Asn Asn Pro Ser Asn Lys Leu Val Ser Thr	305		310		315
Ser Asn Thr Val Thr Ala Ala His Ile Lys Lys Phe Thr Phe Val	320		325		330
Cys Met Ala Leu Ser Leu Thr Leu Cys Phe Val Met Phe Trp Thr	335		340		345

Pro Asn Val Ser	Glu Lys Ile Leu Ile	Asp Ile Ile Gly Val Asp
350		355 360
Phe Ala Phe Ala	Glu Leu Cys Val Val	Pro Leu Arg Ile Phe Ser
365		370 375
Phe Phe Pro Val	Pro Val Thr Val Arg	Ala His Leu Thr Gly Trp
380		385 390
Leu Met Thr Leu	Lys Lys Thr Phe Val	Leu Ala Pro Ser Ser Val
395		400 405
Leu Arg Ile Ile	Val Leu Ile Ala Ser	Leu Val Val Leu Pro Tyr
410		415 420
Leu Gly Val His	Gly Ala Thr Leu Gly	Val Gly Ser Leu Leu Ala
425		430 435
Gly Phe Val Gly	Glu Ser Thr Met Val	Ala Ile Ala Ala Cys Tyr
440		445 450
Val Tyr Arg Lys	Gln Lys Lys Lys Met	Glu Asn Glu Ser Ala Thr
455		460 465
Glu Gly Glu Asp	Ser Ala Met Thr Asp	Met Pro Pro Thr Glu Glu
470		475 480
Val Thr Asp Ile	Val Glu Met Arg Glu	Glu Asn Glu
485		490

<210> 8
 <211> 535
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 33, 66, 96, 387
 <223> unknown base

<400> 8
 cctgacagaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50
 tgagcttctg gtgccttttg gctctaattc tggccacaca gagaancagt 100
 cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150
 agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200
 tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250
 aagaataacc ccagcaaca actggtgagc acgagcaaca cagtcacggc 300
 ggccacatc aagaagttca ccttcgtctg catggctctg tcaactcagc 350
 tctgtttcgt gatgttttgg acacccaacg tgtctgngaa aatcttgata 400
 gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccttt 450

gcggatcttc tccttcttcc cagttccagt cacagtgagg gcgcattctca 500

ccgggtgggt gatgacactg aagaaaacct tcgtc 535

<210> 9

<211> 434

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,
293, 296, 305, 336, 358, 361

<223> unknown base

<400> 9

tgacggaatc ccgggctggg tatcctggtt tngacaagat aaacccccag 50

caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100

agttcacctt ngtttgnatg gntctgtcaa ctacacgtnt gtttcgtgat 150

gttttgagaca cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200

tggantttgc ctttgcagaa ntttgngntg ttccctttgcg gattttctcc 250

tttttcccag ttccagtcac agngaggcg catctcaccg ggnggntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcgggatca 350

ttgtcctnat ngccagcctt gtggtcctac cctacctggg ggtgcacggt 400

gcgaccctgg gcgtgggttc cctcctggcg ggca 434

<210> 10

<211> 154

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 33, 49, 68, 83, 90, 98, 119

<223> unknown base

<400> 10

tattccagtc tccggtcacg gggagggcgc atntcaccgg gtggctgang 50

acactgaaga aaaccttngt ccttgcccc agntttgtgn tgcggatnat 100

cgctcctcatc gccagcctng tggctctacc ctacctgggg gtgcacggtg 150

agac 154

<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 11
ctgatccggt tcttggtgcc cctg 24

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
gctctgtcac tcacgctc 18

<210> 13
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 13
tcattctcttc cctctccc 18

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 14
ccttccgccca cggagttc 18

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 15
ggcaaagtcc actccgatga tgct 24

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 16
gcctgctgtg gtcacaggtc tccg 24

<210> 17

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 17

tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18

<211> 1901

<212> DNA

<213> Homo sapiens

<400> 18

gccccgcgcc cggcgccggg cgcccgaagc cgggagccac cgccatgggg 50

gcctgcctgg gagcctgctc cctgctcagc tgcgcgtcct gcctctgcgg 100

ctctgcccc tgcctcctgt gcagctgctg ccccgccagc cgcaactcca 150

ccgtgagccg cctcatcttc acgttcttcc tcttctggtg ggtgctggtg 200

tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250

ctgggtgtgt gaggaggggg ccgggatccc caccgtcctg cagggccaca 300

tcgactgtgg ctccctgctt ggctaccgcy ctgtctaccg catgtgcttc 350

gccacggcgg ccttcttctt cttctttttc accctgctca tgcctctgct 400

gagcagcagc cgggaccccc gggctgccat ccagaatggg ttttggttct 450

ttaagttcct gatcctggtg ggcctcaccg tgggtgcctt ctacatccct 500

gacggctcct tcaccaacat ctggttctac ttggcgctcg tgggctcctt 550

cctcttcctc ctcatccagc tgggtgctgct catcgacttt gcgcactcct 600

ggaaccagcg gtggctgggc aaggccgagg agtgcgattc ccgtgcctgg 650

tacgcaggcc tcttcttctt cactctcttc ttctacttgc tgtcgatcgc 700

ggccgtggcg ctgatgttca tgtactacac tgagcccagc ggctgccacg 750

agggcaaggt ctcatcagc ctcaacctca ccttctgtgt ctgcgtgtcc 800

atcgctgctg tcctgcccc ggtccaggac gccagccca actcgggtct 850

gctgcaggcc tcggatcatca cctctacac catgtttgtc acctggtcag 900

ccctatccag tatccctgaa cagaaatgca accccattt gccaacccag 950

ctgggcaacg agacagttgt ggcaggcccc gagggctatg agacccagtg 1000
 gtgggatgcc cagagcattg tgggcctcat catcttcctc ctgtgcaccc 1050
 tcttcatcag totgcgctcc tcagaccacc ggcaggtgaa cagcctgatg 1100
 cagaccgagg agtgcgccacc tatgctagac gccacacagc agcagcagca 1150
 gcaggtggca gcctgtgagg gccgggcctt tgacaacgag caggacggcg 1200
 tcacctacag ctactccttc ttccacttct gcctggtgct ggctcactg 1250
 caggtcatga tgacgctcac caactggtac aagcccgggtg agacccggaa 1300
 gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350
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 aaccgcgact tcagctgagg cagcctcaca gcctgccatc tgggtgcctcc 1450
 tgccacctgg tgcctctcgg ctcggtgaca gccaacctgc cccctcccca 1500
 caccaatcag ccaggctgag cccccacccc tgccccagct ccaggacctg 1550
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 ggggaactcc caccacagtg gggcatccgg cactgaagcc ctggtgttcc 1800
 tggtcacgtc ccccagggga cctgcccc ttctggact tcgtgcctta 1850
 ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900
 a 1901

<210> 19

<211> 457

<212> PRT

<213> Homo sapiens

<400> 19

Met	Gly	Ala	Cys	Leu	Gly	Ala	Cys	Ser	Leu	Leu	Ser	Cys	Ala	Ser
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Cys	Leu	Cys	Gly	Ser	Ala	Pro	Cys	Ile	Leu	Cys	Ser	Cys	Cys	Pro
			20						25					30
Ala	Ser	Arg	Asn	Ser	Thr	Val	Ser	Arg	Leu	Ile	Phe	Thr	Phe	Phe
			35						40					45
Leu	Phe	Leu	Gly	Val	Leu	Val	Ser	Ile	Ile	Met	Leu	Ser	Pro	Gly
			50						55					60

Val	Glu	Ser	Gln	Leu	Tyr	Lys	Leu	Pro	Trp	Val	Cys	Glu	Glu	Gly	65	70	75
Ala	Gly	Ile	Pro	Thr	Val	Leu	Gln	Gly	His	Ile	Asp	Cys	Gly	Ser	80	85	90
Leu	Leu	Gly	Tyr	Arg	Ala	Val	Tyr	Arg	Met	Cys	Phe	Ala	Thr	Ala	95	100	105
Ala	Phe	Phe	Phe	Phe	Phe	Phe	Thr	Leu	Leu	Met	Leu	Cys	Val	Ser	110	115	120
Ser	Ser	Arg	Asp	Pro	Arg	Ala	Ala	Ile	Gln	Asn	Gly	Phe	Trp	Phe	125	130	135
Phe	Lys	Phe	Leu	Ile	Leu	Val	Gly	Leu	Thr	Val	Gly	Ala	Phe	Tyr	140	145	150
Ile	Pro	Asp	Gly	Ser	Phe	Thr	Asn	Ile	Trp	Phe	Tyr	Phe	Gly	Val	155	160	165
Val	Gly	Ser	Phe	Leu	Phe	Ile	Leu	Ile	Gln	Leu	Val	Leu	Leu	Ile	170	175	180
Asp	Phe	Ala	His	Ser	Trp	Asn	Gln	Arg	Trp	Leu	Gly	Lys	Ala	Glu	185	190	195
Glu	Cys	Asp	Ser	Arg	Ala	Trp	Tyr	Ala	Gly	Leu	Phe	Phe	Phe	Thr	200	205	210
Leu	Leu	Phe	Tyr	Leu	Leu	Ser	Ile	Ala	Ala	Val	Ala	Leu	Met	Phe	215	220	225
Met	Tyr	Tyr	Thr	Glu	Pro	Ser	Gly	Cys	His	Glu	Gly	Lys	Val	Phe	230	235	240
Ile	Ser	Leu	Asn	Leu	Thr	Phe	Cys	Val	Cys	Val	Ser	Ile	Ala	Ala	245	250	255
Val	Leu	Pro	Lys	Val	Gln	Asp	Ala	Gln	Pro	Asn	Ser	Gly	Leu	Leu	260	265	270
Gln	Ala	Ser	Val	Ile	Thr	Leu	Tyr	Thr	Met	Phe	Val	Thr	Trp	Ser	275	280	285
Ala	Leu	Ser	Ser	Ile	Pro	Glu	Gln	Lys	Cys	Asn	Pro	His	Leu	Pro	290	295	300
Thr	Gln	Leu	Gly	Asn	Glu	Thr	Val	Val	Ala	Gly	Pro	Glu	Gly	Tyr	305	310	315
Glu	Thr	Gln	Trp	Trp	Asp	Ala	Pro	Ser	Ile	Val	Gly	Leu	Ile	Ile	320	325	330
Phe	Leu	Leu	Cys	Thr	Leu	Phe	Ile	Ser	Leu	Arg	Ser	Ser	Asp	His	335	340	345
Arg	Gln	Val	Asn	Ser	Leu	Met	Gln	Thr	Glu	Glu	Cys	Pro	Pro	Met			

	350		355		360
Leu Asp Ala Thr	Gln Gln Gln Gln Gln	Gln Val Ala Ala Cys Glu			
	365		370		375
Gly Arg Ala Phe	Asp Asn Glu Gln Asp	Gly Val Thr Tyr Ser Tyr			
	380		385		390
Ser Phe Phe His	Phe Cys Leu Val Leu	Ala Ser Leu His Val Met			
	395		400		405
Met Thr Leu Thr	Asn Trp Tyr Lys Pro	Gly Glu Thr Arg Lys Met			
	410		415		420
Ile Ser Thr Trp	Thr Ala Val Trp Val	Lys Ile Cys Ala Ser Trp			
	425		430		435
Ala Gly Leu Leu	Leu Tyr Leu Trp Thr	Leu Val Ala Pro Leu Leu			
	440		445		450
Leu Arg Asn Arg	Asp Phe Ser				
	455				

<210> 20
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 20
 gccgcctcat cttcacgttc ttcc 24

 <210> 21
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 21
 tcatocagct ggtgctgctc 20

 <210> 22
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 22
 cttcttccac ttctgcctgg 20

 <210> 23
 <211> 18

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 23
cctgggcaaa aatgcaac 18

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
caggaatgta gaaggcaccc acgg 24

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
tggcacagat cttcacccac acgg 24

<210> 26
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
tgtccatcat tatgctgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27
<211> 1351
<212> DNA
<213> Homo sapiens

<400> 27
gagcgaggcc ggggactgaa ggtgtgggtg tcgagccctc tggcagaggg 50
ttaacctggg tcaaatgcac ggattctcac ctggtacagt tacgctctcc 100
cgcggcacgt ccgcgaggac ttgaagtcct gagcgctcaa gtttgtccgt 150
aggtcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200
tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250

actgccgatt cggaagtcct tgaggagcgt cagaagcggc ttccctacgt 300
 cccagagccc tattaccggy aatctggatg ggaccgcctc cgggagctgt 350
 ttggcaaaga tgaacagcag agaatttcaa aggaccttgc taatatctgt 400
 aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450
 agctttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500
 tttatcataa ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca 550
 cgaggcttca ttcgttatgg ctggcgctgg ggttgagaaa ctgcagtgtt 600
 tgtgactata ttcaacacag tgaacactag tctgaatgta taccgaaata 650
 aagatgcctt aagccatttt gtaattgcag gagctgtcac gggaagtctt 700
 tttaggataa acgtaggcct gcgtggcctg gtggctggtg gcataattgg 750
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 cctccctgag aaaattgaaa gtagtttacg ggaagatgaa cctgagaatg 950
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 gtactctcac ttactttatc cttaaattta aatacatact tatgtttgta 1250
 ttaatctatc aatatatgca tacatggata tatccaccca cctagatttt 1300
 aagcagtaaa taaaacattt cgcaaaagat taaagttgaa ttttacagtt 1350
 t 1351

<210> 28

<211> 285

<212> PRT

<213> Homo sapiens

<400> 28

Met	Glu	Val	Pro	Pro	Pro	Ala	Pro	Arg	Ser	Phe	Leu	Cys	Arg	Ala
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Leu	Cys	Leu	Phe	Pro	Arg	Val	Phe	Ala	Ala	Glu	Ala	Val	Thr	Ala
				20				25						30

Asp	Ser	Glu	Val	Leu	Glu	Glu	Arg	Gln	Lys	Arg	Leu	Pro	Tyr	Val	35	40	45
Pro	Glu	Pro	Tyr	Tyr	Pro	Glu	Ser	Gly	Trp	Asp	Arg	Leu	Arg	Glu	50	55	60
Leu	Phe	Gly	Lys	Asp	Glu	Gln	Gln	Arg	Ile	Ser	Lys	Asp	Leu	Ala	65	70	75
Asn	Ile	Cys	Lys	Thr	Ala	Ala	Thr	Ala	Gly	Ile	Ile	Gly	Trp	Val	80	85	90
Tyr	Gly	Gly	Ile	Pro	Ala	Phe	Ile	His	Ala	Lys	Gln	Gln	Tyr	Ile	95	100	105
Glu	Gln	Ser	Gln	Ala	Glu	Ile	Tyr	His	Asn	Arg	Phe	Asp	Ala	Val	110	115	120
Gln	Ser	Ala	His	Arg	Ala	Ala	Thr	Arg	Gly	Phe	Ile	Arg	Tyr	Gly	125	130	135
Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	140	145	150
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	155	160	165
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	170	175	180
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	185	190	195
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	200	205	210
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	215	220	225
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	230	235	240
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	245	250	255
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	260	265	270
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	275	280	285

<210> 29

<211> 324

<212> DNA

<213> Homo sapiens

<400> 29

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ctattacccg gaatctggat gggaccgctc cgggagctgt ttggcaaaga 100
 tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150
 ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200
 catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250
 ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300
 ttcgttcattg gctggcgccg aacc 324

<210> 30
 <211> 377
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 262, 330, 371
 <223> unknown base

<400> 30
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 accgcggagc ttttttctgt agagcattgt gcctatttcc ccgagttttt 100
 gctgccgaag ctgtgactgc cgattcggaa gtccttgagg agcgtcagaa 150
 gcggcttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200
 gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250
 cttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300
 gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350
 agagccaggc agaaatttat nataacc 377

<210> 31
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 31
 tcgtacagtt acgctctccc 20

<210> 32
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 32
cttgaggagc gtcagaagcg 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
ataacgaatg aagcctcgtg 20

<210> 34
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 34
gctaatatct gtaagacggc agctacagca ggcatcattg 40

<210> 35
<211> 1819
<212> DNA
<213> Homo sapiens

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ccaccacagt ctgcgttget gccccgcctg ggccaggccc caaaggcaag 100
gacaaagcag ctgtcaggga acctccgccg gagtccaatt tacgtgcagc 150
tgccggcaac cacaggttcc aagatggttt gcgggggctt cgcgtgttcc 200
aagaactgcc tgtgcgccct caacctgctt tacaccttgg ttagtctgct 250
gctaattgga attgctgcgt ggggcattgg cttcgggctg atttccagtc 300
tccgagtggc cggcgtggtc attgcagtgg gcatcttctt gttcctgatt 350
gctttagtgg gtctgattgg agctgtaaaa catcatcagg tgttgctatt 400
tttttatatg attattctgt tacttgtatt tattgttcag ttttctgtat 450
cttgcgcttg tttagccctg aaccaggagc aacagggcca gcttctggag 500
gttggttgga acaatacggc aagtgcctga aatgacatcc agagaaatct 550
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gctgtgttaa aagtgaccac tcgtgctcgc catgtgctcc aatcatagga 650
gaatatgctg gagaggtttt gagatttggt ggtggcattg gcctgttctt 700

cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750
 agaaagaccc ccgcgcgaat cctagtgcac tcctttgatg agaaaacaag 800
 gaagatttcc ttctgtatta tgatcttggt cactttctgt aattttctgt 850
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<210> 36

<211> 204

<212> PRT

<213> Homo sapiens

<400> 36

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Leu	Asn	Leu	Leu	Tyr	Thr	Leu	Val	Ser	Leu	Leu	Leu	Ile	Gly	Ile
				20					25					30

Ala	Ala	Trp	Gly	Ile	Gly	Phe	Gly	Leu	Ile	Ser	Ser	Leu	Arg	Val	35	40	45
Val	Gly	Val	Val	Ile	Ala	Val	Gly	Ile	Phe	Leu	Phe	Leu	Ile	Ala	50	55	60
Leu	Val	Gly	Leu	Ile	Gly	Ala	Val	Lys	His	His	Gln	Val	Leu	Leu	65	70	75
Phe	Phe	Tyr	Met	Ile	Ile	Leu	Leu	Leu	Val	Phe	Ile	Val	Gln	Phe	80	85	90
Ser	Val	Ser	Cys	Ala	Cys	Leu	Ala	Leu	Asn	Gln	Glu	Gln	Gln	Gly	95	100	105
Gln	Leu	Leu	Glu	Val	Gly	Trp	Asn	Asn	Thr	Ala	Ser	Ala	Arg	Asn	110	115	120
Asp	Ile	Gln	Arg	Asn	Leu	Asn	Cys	Cys	Gly	Phe	Arg	Ser	Val	Asn	125	130	135
Pro	Asn	Asp	Thr	Cys	Leu	Ala	Ser	Cys	Val	Lys	Ser	Asp	His	Ser	140	145	150
Cys	Ser	Pro	Cys	Ala	Pro	Ile	Ile	Gly	Glu	Tyr	Ala	Gly	Glu	Val	155	160	165
Leu	Arg	Phe	Val	Gly	Gly	Ile	Gly	Leu	Phe	Phe	Ser	Phe	Thr	Glu	170	175	180
Ile	Leu	Gly	Val	Trp	Leu	Thr	Tyr	Arg	Tyr	Arg	Asn	Gln	Lys	Asp	185	190	195
Pro	Arg	Ala	Asn	Pro	Ser	Ala	Phe	Leu							200		

<210> 37
 <211> 390
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> unsure
 <222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336
 <223> unknown base

<400> 37
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 tagccntgaa ccaggagcaa cagggtcagn ttntggaggt tggttggaac 150
 aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200
 gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250
 gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300

gagggttttga gatttggttg tggcattggc ctgttnttca gttttacaga 350

gacctgggt gtttggtga cctacagata caggaaccag 390

<210> 38

<211> 566

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 27

<223> unknown base

<400> 38

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ttacaccaat gtattctaga atagttagt cttaggaaat tgtggtttta 150

tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200

tctaattgtat aataacattt accttcagcc tcccatcaga atggaacgag 250

ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300

taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgag 350

ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400

cggttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450

gcatatttga atatgatctc ccataatttg aaattgaaat cgtatttgtgt 500

ggaggaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550

gttgtgcccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 84-85, 206

<223> unknown base

<400> 39

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cttgtttagc ccctgaaacc aggagcaaca gggnnacagc tcttgagggt 100

tggttgcaa caatcacggc caagtgaact cgcaaatgac atcccagaga 150

aatcctaaac tgctgtgggt tccgaagtgt taacccaaat gacacctgtc 200

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    ataggagaat atgc 264

<210> 40
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 40
    acccacgtct gcgttgctgc c 21

<210> 41
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 41
    gagaatatgc tggagagg 18

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 42
    aggaatgcac taggattcgc gcgg 24

<210> 43
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
    ggccccaaag gcaaggacaa agcagctgtc agggaacctc cgccg 45

<210> 44
<211> 2061
<212> DNA
<213> Homo sapiens

<400> 44
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    tcccttggtg tgctctgggt ggcccagatg ctactggctg ccagttttga 100

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gacgctgcag tgtgagggac ctgtctgcac tgaggagagc agctgccaca 150
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 tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggctgat 250
 cctccaaggt ccagccaagc cagtttttga aggggacctg ctggttctgc 300
 gctgccaggc ctggcaagac tggccactga ctcaggtgac cttctaccga 350
 gatggctcag ctctgggtcc ccccgggcct aacagggaat tctccatcac 400
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 ttgtagccta a 2061

<210> 45
 <211> 359
 <212> PRT
 <213> Homo sapiens

<400> 45

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Glu	Thr	Leu	Gln	Cys	Glu	Gly	Pro	Val	Cys	Thr	Glu	Glu	Ser	Ser	35	40	45	
Cys	His	Thr	Glu	Asp	Asp	Leu	Thr	Asp	Ala	Arg	Glu	Ala	Gly	Phe	50	55	60	
Gln	Val	Lys	Ala	Tyr	Thr	Phe	Ser	Glu	Pro	Phe	His	Leu	Ile	Val	65	70	75	
Ser	Tyr	Asp	Trp	Leu	Ile	Leu	Gln	Gly	Pro	Ala	Lys	Pro	Val	Phe	80	85	90	
Glu	Gly	Asp	Leu	Leu	Val	Leu	Arg	Cys	Gln	Ala	Trp	Gln	Asp	Trp	95	100	105	
Pro	Leu	Thr	Gln	Val	Thr	Phe	Tyr	Arg	Asp	Gly	Ser	Ala	Leu	Gly	110	115	120	
Pro	Pro	Gly	Pro	Asn	Arg	Glu	Phe	Ser	Ile	Thr	Val	Val	Gln	Lys	125	130	135	
Ala	Asp	Ser	Gly	His	Tyr	His	Cys	Ser	Gly	Ile	Phe	Gln	Ser	Pro	140	145	150	

Gly	Pro	Gly	Ile	Pro	Glu	Thr	Ala	Ser	Val	Val	Ala	Ile	Thr	Val	155	160	165
Gln	Glu	Leu	Phe	Pro	Ala	Pro	Ile	Leu	Arg	Ala	Val	Pro	Ser	Ala	170	175	180
Glu	Pro	Gln	Ala	Gly	Ser	Pro	Met	Thr	Leu	Ser	Cys	Gln	Thr	Lys	185	190	195
Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	200	205	210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	215	220	225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	230	235	240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	245	250	255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	260	265	270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	275	280	285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	290	295	300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	305	310	315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	320	325	330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	335	340	345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		350	355	

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

tgggctgtgt cctcatgg 18

<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 47
tttccagcgc caattctc 18

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
agttcttgga ctgtgatagc cac 23

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 49
aaacttggtt gtcctcagtg gctg 24

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 50
gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51
<211> 2181
<212> DNA
<213> Homo sapiens

<400> 51
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ccaccagaag tttgagcctc tttggtagca ggaggctgga agaaaggaca 100
gaagtagctc tggctgtgat ggggatctta ctgggcctgc tactcctggg 150
gcacctaaca gtggacactt atggccgtcc catcctggaa gtgccagaga 200
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<210> 52
 <211> 321
 <212> PRT
 <213> Homo sapiens

<400> 52

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Gly	Pro	Trp	Lys	Gly	Asp	Val	Asn	Leu	Pro	Cys	Thr	Tyr	Asp	Pro
				35					40					45
Leu	Gln	Gly	Tyr	Thr	Gln	Val	Leu	Val	Lys	Trp	Ile	Val	Gln	Arg
				50					55					60
Gly	Ser	Asp	Pro	Val	Thr	Ile	Phe	Leu	Arg	Asp	Ser	Ser	Gly	Asp
				65					70					75
His	Ile	Gln	Gln	Ala	Lys	Tyr	Gln	Gly	Arg	Leu	His	Val	Ser	His
				80					85					90
Lys	Val	Pro	Gly	Asp	Val	Ser	Leu	Gln	Leu	Ser	Thr	Leu	Glu	Met
				95					100					105
Asp	Asp	Arg	Ser	His	Tyr	Thr	Cys	Glu	Val	Thr	Trp	Gln	Thr	Pro
				110					115					120
Asp	Gly	Asn	Gln	Val	Val	Arg	Asp	Lys	Ile	Thr	Glu	Leu	Arg	Val
				125					130					135
Gln	Lys	Leu	Ser	Val	Ser	Lys	Pro	Thr	Val	Thr	Thr	Gly	Ser	Gly
				140					145					150
Tyr	Gly	Phe	Thr	Val	Pro	Gln	Gly	Met	Arg	Ile	Ser	Leu	Gln	Cys
				155					160					165
Gln	Ala	Arg	Gly	Ser	Pro	Pro	Ile	Ser	Tyr	Ile	Trp	Tyr	Lys	Gln
				170					175					180

Gln	Thr	Asn	Asn	Gln	Glu	Pro	Ile	Lys	Val	Ala	Thr	Leu	Ser	Thr
				185					190					195
Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser	Tyr	Phe
				200					205					210
Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	Ile
				215					220					225
Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys
				230					235					240
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser
				245					250					255
Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr
				260					265					270
Leu	Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe
				275					280					285
Ala	Ile	Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr
				290					295					300
Met	Ala	Tyr	Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His
				305					310					315
Val	Tyr	Glu	Ala	Ala	Arg									
				320										

<210> 53

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 53

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<210> 54

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 54

gtcgggaagac atcccaacaa g 21

<210> 55

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 55

cttcacaatg tcgctgtgct gctc 24

<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 56

agccaaatcc agcagctggc ttac 24

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 57

tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58

<211> 2458

<212> DNA

<213> Homo sapiens

<400> 58

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cgcccggcac atggctgcag ccacctcgcg cgcaccccga ggcgcgcgc 100

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ccttctcctc ttgctagttt cctactatgt tggaaccttg gggactcaca 250

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<210> 59
 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 59

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Val	Thr	Leu	Pro	Cys	His	His	Gln	Leu	Gly	Leu	Pro	Glu	Lys	Asp
				35					40					45
Thr	Leu	Asp	Ile	Glu	Trp	Leu	Leu	Thr	Asp	Asn	Glu	Gly	Asn	Gln
				50					55					60
Lys	Val	Val	Ile	Thr	Tyr	Ser	Ser	Arg	His	Val	Tyr	Asn	Asn	Leu
				65					70					75
Thr	Glu	Glu	Gln	Lys	Gly	Arg	Val	Ala	Phe	Ala	Ser	Asn	Phe	Leu
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Ala	Gly	Asp	Ala	Ser	Leu	Gln	Ile	Glu	Pro	Leu	Lys	Pro	Ser	Asp
				95					100					105
Glu	Gly	Arg	Tyr	Thr	Cys	Lys	Val	Lys	Asn	Ser	Gly	Arg	Tyr	Val
				110					115					120
Trp	Ser	His	Val	Ile	Leu	Lys	Val	Leu	Val	Arg	Pro	Ser	Lys	Pro
				125					130					135
Lys	Cys	Glu	Leu	Glu	Gly	Glu	Leu	Thr	Glu	Gly	Ser	Asp	Leu	Thr
				140					145					150
Leu	Gln	Cys	Glu	Ser	Ser	Ser	Gly	Thr	Glu	Pro	Ile	Val	Tyr	Tyr
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Trp	Gln	Arg	Ile	Arg	Glu	Lys	Glu	Gly	Glu	Asp	Glu	Arg	Leu	Pro
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<210> 62

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 62

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<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

<400> 63

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 attaataaac attaggtggt tgttaaaaaa aaaa 3534

<210> 64
 <211> 655
 <212> PRT
 <213> Homo sapiens
 <400> 64
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 Arg Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu
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Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	50	55	60
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	65	70	75
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	80	85	90
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys	95	100	105
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	110	115	120
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro	125	130	135
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys	140	145	150
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp	155	160	165
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro	170	175	180
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln	185	190	195
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val	200	205	210
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	215	220	225
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu	230	235	240
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu	245	250	255
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile	260	265	270
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys	275	280	285
Glu	Asp	Val	Asn	Lys	Thr	Leu	Pro	Asn	Leu	Gln	Val	Val	Asn	His	290	295	300
Gln	Gln	Gly	Pro	His	His	Arg	His	Ile	Leu	Lys	Leu	Leu	Pro	Ser	305	310	315
Met	Glu	Ala	Thr	Gly	Gly	Glu	Lys	Ser	Ser	Thr	Pro	Ile	Lys	Gly			

Pro Lys Arg Gly His	320	Pro Arg Gln Asn	325	Leu His Lys His Phe	330
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Ile Asn Glu His	350	Pro Trp Met Ile	355	Val Leu Phe Leu Leu	360
365		370		375	
Val Leu Val Val	380	Pro Arg Gln Asp	385	Pro Ser Ala Ile Val	390
395		400		405	
Lys Trp Ile Tyr	410	Gly Ile Asp Ile Leu	415	Lys	420
425		430		435	
Phe Leu Cys Asn	440	Val Ala Ala Phe Ser	445	Asn	450
455		460		465	
Trp Thr Ile Arg	470	Leu Ala Gln Leu Ile	475	Ser	480
485		490		495	
Gly Leu Met Glu	500	Glu Thr Asp Lys Leu	505	Ala	510
515		520		525	
Pro Asn Ala Lys	530	Leu Leu Thr Val Glu	535	Pro	540
545		550		555	
Pro Leu Leu Arg	560	Ser Gly Ser Ser Ala	565	Leu	570
575		580		585	
Leu Arg Gln Val	590	Asp Leu Gln Pro Ile	595	Phe	600
605		610		615	

Glu	Glu	Ile	Pro	Gln	Ala	Glu	Asp	Lys	Leu	Asp	Arg	Leu	Phe	Glu
				620					625					630
Ile	Ile	Gly	Val	Lys	Ser	Gln	Glu	Ala	Ser	Gln	Thr	Leu	Leu	Asp
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Ser	Val	Tyr	Ser	His	Leu	Pro	Asp	Leu	Leu					
				650					655					

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 65
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<210> 66
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 66
 accgcacatc ctcaagtctt gtcc 24

<210> 67
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 67
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<210> 68
 <211> 2412
 <212> DNA
 <213> Homo sapiens

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<210> 69
 <211> 453
 <212> PRT
 <213> Homo sapiens

<400> 69
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 35 40 45
 Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile
 50 55 60
 Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly
 65 70 75
 Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala
 80 85 90
 Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr
 95 100 105
 Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe

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Thr Ala Ala Ser	Trp Lys Thr Met Cys	Ser Asp Asp Trp Lys Gly	125 130 135
His Tyr Ala Asn	Val Ala Cys Ala Gln	Leu Gly Phe Pro Ser Tyr	140 145 150
Val Ser Ser Asp	Asn Leu Arg Val Ser	Ser Leu Glu Gly Gln Phe	155 160 165
Arg Glu Glu Phe	Val Ser Ile Asp His	Leu Leu Pro Asp Asp Lys	170 175 180
Val Thr Ala Leu	His His Ser Val Tyr	Val Arg Glu Gly Cys Ala	185 190 195
Ser Gly His Val	Val Thr Leu Gln Cys	Thr Ala Cys Gly His Arg	200 205 210
Arg Gly Tyr Ser	Ser Arg Ile Val Gly	Gly Asn Met Ser Leu Leu	215 220 225
Ser Gln Trp Pro	Trp Gln Ala Ser Leu	Gln Phe Gln Gly Tyr His	230 235 240
Leu Cys Gly Gly	Ser Val Ile Thr Pro	Leu Trp Ile Ile Thr Ala	245 250 255
Ala His Cys Val	Tyr Asp Leu Tyr Leu	Pro Lys Ser Trp Thr Ile	260 265 270
Gln Val Gly Leu	Val Ser Leu Leu Asp	Asn Pro Ala Pro Ser His	275 280 285
Leu Val Glu Lys	Ile Val Tyr His Ser	Lys Tyr Lys Pro Lys Arg	290 295 300
Leu Gly Asn Asp	Ile Ala Leu Met Lys	Leu Ala Gly Pro Leu Thr	305 310 315
Phe Asn Glu Met	Ile Gln Pro Val Cys	Leu Pro Asn Ser Glu Glu	320 325 330
Asn Phe Pro Asp	Gly Lys Val Cys Trp	Thr Ser Gly Trp Gly Ala	335 340 345
Thr Glu Asp Gly	Gly Asp Ala Ser Pro	Val Leu Asn His Ala Ala	350 355 360
Val Pro Leu Ile	Ser Asn Lys Ile Cys	Asn His Arg Asp Val Tyr	365 370 375
Gly Gly Ile Ile	Ser Pro Ser Met Leu	Cys Ala Gly Tyr Leu Thr	380 385 390
Gly Gly Val Asp	Ser Cys Gln Gly Asp	Ser Gly Gly Pro Leu Val	395 400 405

Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe
410 415 420

Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg
425 430 435

Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu Arg Asp
440 445 450

Leu Lys Thr

<210> 70

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

tgacatcgcc cttatgaagc tggc 24

<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71

tacacgtccc tgtggttgca gata 24

<210> 72

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 72

cgttcaatgc agaaatgata cagcctgtgt gcctgcccaa ctctgaagag 50

<210> 73

<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

cccacgcgtc cgtcctagtc cccggggccaa ctcgacagc ttgctcattt 50

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 <211> 735
 <212> PRT
 <213> Homo sapiens

<400> 74
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 Val Ser Leu Trp Asn Gln Gly Arg Ala Asp Glu Val Val Ser Ala
 35 40 45
 Ser Val Arg Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp
 50 55 60
 Ser Lys Asn His Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu
 65 70 75
 Ser Lys Glu Leu Ile Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile
 80 85 90
 Ala Ser Ser Phe Thr Glu Thr His Tyr Leu Gln Asp Gly Thr Asp
 95 100 105
 Val Ser Leu Ala Arg Asn Tyr Thr Gly His Cys Tyr Tyr His Gly
 110 115 120
 His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys
 125 130 135
 Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val
 140 145 150
 Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro
 155 160 165
 Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His
 170 175 180
 Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser
 185 190 195
 Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr
 200 205 210

Lys Tyr Val Glu	Leu Val Ile Val Ala	Asp Asn Arg Glu Phe	Gln
215		220	225
Arg Gln Gly Lys	Asp Leu Glu Lys Val	Lys Gln Arg Leu Ile	Glu
230		235	240
Ile Ala Asn His	Val Asp Lys Phe Tyr	Arg Pro Leu Asn Ile	Arg
245		250	255
Ile Val Leu Val	Gly Val Glu Val Trp	Asn Asp Met Asp Lys	Cys
260		265	270
Ser Val Ser Gln	Asp Pro Phe Thr Ser	Leu His Glu Phe Leu	Asp
275		280	285
Trp Arg Lys Met	Lys Leu Leu Pro Arg	Lys Ser His Asp Asn	Ala
290		295	300
Gln Leu Val Ser	Gly Val Tyr Phe Gln	Gly Thr Thr Ile Gly	Met
305		310	315
Ala Pro Ile Met	Ser Met Cys Thr Ala	Asp Gln Ser Gly Gly	Ile
320		325	330
Val Met Asp His	Ser Asp Asn Pro Leu	Gly Ala Ala Val Thr	Leu
335		340	345
Ala His Glu Leu	Gly His Asn Phe Gly	Met Asn His Asp Thr	Leu
350		355	360
Asp Arg Gly Cys	Ser Cys Gln Met Ala	Val Glu Lys Gly Gly	Cys
365		370	375
Ile Met Asn Ala	Ser Thr Gly Tyr Pro	Phe Pro Met Val Phe	Ser
380		385	390
Ser Cys Ser Arg	Lys Asp Leu Glu Thr	Ser Leu Glu Lys Gly	Met
395		400	405
Gly Val Cys Leu	Phe Asn Leu Pro Glu	Val Arg Glu Ser Phe	Gly
410		415	420
Gly Gln Lys Cys	Gly Asn Arg Phe Val	Glu Glu Gly Glu Glu	Cys
425		430	435
Asp Cys Gly Glu	Pro Glu Glu Cys Met	Asn Arg Cys Cys Asn	Ala
440		445	450
Thr Thr Cys Thr	Leu Lys Pro Asp Ala	Val Cys Ala His Gly	Leu
455		460	465
Cys Cys Glu Asp	Cys Gln Leu Lys Pro	Ala Gly Thr Ala Cys	Arg
470		475	480
Asp Ser Ser Asn	Ser Cys Asp Leu Pro	Glu Phe Cys Thr Gly	Ala
485		490	495
Ser Pro His Cys	Pro Ala Asn Val Tyr	Leu His Asp Gly His	Ser

500	505	510
Cys Gln Asp Val Asp Gly Tyr Cys Tyr	Asn Gly Ile Cys Gln Thr	
515	520	525
His Glu Gln Gln Cys Val Thr Leu Trp	Gly Pro Gly Ala Lys Pro	
530	535	540
Ala Pro Gly Ile Cys Phe Glu Arg Val	Asn Ser Ala Gly Asp Pro	
545	550	555
Tyr Gly Asn Cys Gly Lys Val Ser Lys	Ser Ser Phe Ala Lys Cys	
560	565	570
Glu Met Arg Asp Ala Lys Cys Gly Lys	Ile Gln Cys Gln Gly Gly	
575	580	585
Ala Ser Arg Pro Val Ile Gly Thr Asn	Ala Val Ser Ile Glu Thr	
590	595	600
Asn Ile Pro Leu Gln Gln Gly Gly Arg	Ile Leu Cys Arg Gly Thr	
605	610	615
His Val Tyr Leu Gly Asp Asp Met Pro	Asp Pro Gly Leu Val Leu	
620	625	630
Ala Gly Thr Lys Cys Ala Asp Gly Lys	Ile Cys Leu Asn Arg Gln	
635	640	645
Cys Gln Asn Ile Ser Val Phe Gly Val	His Glu Cys Ala Met Gln	
650	655	660
Cys His Gly Arg Gly Val Cys Asn Asn	Arg Lys Asn Cys His Cys	
665	670	675
Glu Ala His Trp Ala Pro Pro Phe Cys	Asp Lys Phe Gly Phe Gly	
680	685	690
Gly Ser Thr Asp Ser Gly Pro Ile Arg	Gln Ala Glu Ala Arg Gln	
695	700	705
Glu Ala Ala Glu Ser Asn Arg Glu Arg	Gly Gln Gly Gln Glu Pro	
710	715	720
Val Gly Ser Gln Glu His Ala Ser Thr	Ala Ser Leu Thr Leu Ile	
725	730	735

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 <221> unsure
 <222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473
 <223> unknown base

 <400> 75

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 ctacccagga agtttgacga aacagtgcaa ggaagggcag ganttcctgg 150
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<211> 27

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 77

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<210> 78

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 78

tacctgcacg atgggcac 18

<210> 79

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 79
cactgggcac ctcccttc 18

<210> 80
<211> 26
<212> DNA
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<220>
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<400> 80
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<210> 81
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<220>
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<400> 81
tccctgttgg actctgcagc ttcc 24

<210> 82
<211> 19
<212> DNA
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<220>
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<400> 82
cttcgctggg aagagtttg 19

<210> 83
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gtgcaaccaa cagatacaaa ctcttcccag cgaagaagct gaaaagcgtc 50

<210> 84
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<212> DNA
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<212> PRT
<213> Homo sapiens

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Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser
35 40 45
Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu
50 55 60
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<400> 86
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<210> 87
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<400> 87
ggtagagatg tagaaggga agcaagacc 29

<210> 88
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<212> DNA
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<223> Synthetic oligonucleotide probe

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<210> 89

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 ttttaa 2956

<210> 90
 <211> 432
 <212> PRT
 <213> Homo sapiens

<400> 90

Met	Pro	Ala	Arg	Pro	Gly	Arg	Leu	Leu	Pro	Leu	Leu	Ala	Arg	Pro	1	5	10	15
Ala	Ala	Leu	Thr	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	His	Gly	Gly	20	25	30	
Gly	Gly	Arg	Trp	Gly	Ala	Arg	Ala	Gln	Glu	Ala	Ala	Ala	Ala	Ala	35	40	45	
Ala	Asp	Gly	Pro	Pro	Ala	Ala	Asp	Gly	Glu	Asp	Gly	Gln	Asp	Pro	50	55	60	
His	Ser	Lys	His	Leu	Tyr	Thr	Ala	Asp	Met	Phe	Thr	His	Gly	Ile	65	70	75	
Gln	Ser	Ala	Ala	His	Phe	Val	Met	Phe	Phe	Ala	Pro	Trp	Cys	Gly	80	85	90	
His	Cys	Gln	Arg	Leu	Gln	Pro	Thr	Trp	Asn	Asp	Leu	Gly	Asp	Lys	95	100	105	
Tyr	Asn	Ser	Met	Glu	Asp	Ala	Lys	Val	Tyr	Val	Ala	Lys	Val	Asp	110	115	120	
Cys	Thr	Ala	His	Ser	Asp	Val	Cys	Ser	Ala	Gln	Gly	Val	Arg	Gly	125	130	135	
Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Lys	Pro	Gly	Gln	Glu	Ala	Val	Lys	140	145	150	
Tyr	Gln	Gly	Pro	Arg	Asp	Phe	Gln	Thr	Leu	Glu	Asn	Trp	Met	Leu	155	160	165	
Gln	Thr	Leu	Asn	Glu	Glu	Pro	Val	Thr	Pro	Glu	Pro	Glu	Val	Glu	170	175	180	

Pro	Pro	Ser	Ala	Pro	Glu	Leu	Lys	Gln	Gly	Leu	Tyr	Glu	Leu	Ser	185	190	195
Ala	Ser	Asn	Phe	Glu	Leu	His	Val	Ala	Gln	Gly	Asp	His	Phe	Ile	200	205	210
Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	Pro	215	220	225
Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	Thr	Val	230	235	240
Lys	Ile	Gly	Lys	Val	Asp	Cys	Thr	Gln	His	Tyr	Glu	Leu	Cys	Ser	245	250	255
Gly	Asn	Gln	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Trp	Phe	Arg	Asp	260	265	270
Gly	Lys	Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser	275	280	285
Leu	Arg	Glu	Tyr	Val	Glu	Ser	Gln	Leu	Gln	Arg	Thr	Glu	Thr	Gly	290	295	300
Ala	Thr	Glu	Thr	Val	Thr	Pro	Ser	Glu	Ala	Pro	Val	Leu	Ala	Ala	305	310	315
Glu	Pro	Glu	Ala	Asp	Lys	Gly	Thr	Val	Leu	Ala	Leu	Thr	Glu	Asn	320	325	330
Asn	Phe	Asp	Asp	Thr	Ile	Ala	Glu	Gly	Ile	Thr	Phe	Ile	Lys	Phe	335	340	345
Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Thr	Leu	Ala	Pro	Thr	Trp	350	355	360
Glu	Glu	Leu	Ser	Lys	Lys	Glu	Phe	Pro	Gly	Leu	Ala	Gly	Val	Lys	365	370	375
Ile	Ala	Glu	Val	Asp	Cys	Thr	Ala	Glu	Arg	Asn	Ile	Cys	Ser	Lys	380	385	390
Tyr	Ser	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Leu	Phe	Arg	Gly	Gly	395	400	405
Lys	Lys	Val	Ser	Glu	His	Ser	Gly	Gly	Arg	Asp	Leu	Asp	Ser	Leu	410	415	420
His	Arg	Phe	Val	Leu	Ser	Gln	Ala	Lys	Asp	Glu	Leu				425	430	

<210> 91

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 91
atgttcttcg cgccctggtg 20

<210> 92

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 92

ccaagccaac acactctaca g 21

<210> 93

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 93

aagtggtcgc cttgtgcaac gtgc 24

<210> 94

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 94

ggtcaaaggg gatatatcgc cac 23

<210> 95

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 95

gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggcca 49

<210> 96

<211> 1016

<212> DNA

<213> Homo sapiens

<400> 96

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aaaccaattt atcctcctgg tactatttct tttgcaaatt cagagtctgg 100

gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150

80	85	90
Thr Gly Pro Ile Gly Lys Lys Gly Asp	Lys Gly Glu Lys Gly Leu	
95	100	105
Leu Gly Ile Pro Gly Glu Lys Gly Lys	Ala Gly Thr Val Cys Asp	
110	115	120
Cys Gly Arg Tyr Arg Lys Phe Val Gly	Gln Leu Asp Ile Ser Ile	
125	130	135
Ala Arg Leu Lys Thr Ser Met Lys Phe	Val Lys Asn Val Ile Ala	
140	145	150
Gly Ile Arg Glu Thr Glu Glu Lys Phe	Tyr Tyr Ile Val Gln Glu	
155	160	165
Glu Lys Asn Tyr Arg Glu Ser Leu Thr	His Cys Arg Ile Arg Gly	
170	175	180
Gly Met Leu Ala Met Pro Lys Asp Glu	Ala Ala Asn Thr Leu Ile	
185	190	195
Ala Asp Tyr Val Ala Lys Ser Gly Phe	Phe Arg Val Phe Ile Gly	
200	205	210
Val Asn Asp Leu Glu Arg Glu Gly Gln	Tyr Met Ser Thr Asp Asn	
215	220	225
Thr Pro Leu Gln Asn Tyr Ser Asn Trp	Asn Glu Gly Glu Pro Ser	
230	235	240
Asp Pro Tyr Gly His Glu Asp Cys Val	Glu Met Leu Ser Ser Gly	
245	250	255
Arg Trp Asn Asp Thr Glu Cys His Leu	Thr Met Tyr Phe Val Cys	
260	265	270
Glu Phe Ile Lys Lys Lys Lys		
275		

<210> 98

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 98

cgctgactat gttgccaaga gtgg 24

<210> 99

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 99

gatgatggag gctccataacc tcag 24

<210> 100

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 100

gtgttcattg gcgtgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101

<211> 2574

<212> DNA

<213> Homo sapiens

<400> 101

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gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200
agggatgttt gcgagcggct ggaaccagac ggtgccgata gaggaagcgg 250
gctccatggc tgccctcctg ctgctgcccc tgctgctgtt gctaccgctg 300
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gcgccctggc cgcggctgcc gccgaccgg aaggtcccga ggggggctgc 450
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ccggagggga cggtgccgcc agaggtggag gagccgccgc ccctctgtca 750
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 cgatgaccaa ggttttctcc gcttccatga tcgtactgga gacaccttca 1900
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 catggcccaa cttgtttatt gcag 2574

<210> 102

<211> 730

<212> PRT

<213> Homo sapiens

<400> 102

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Met	Phe	Ala	Ser	Gly	Trp	Asn	Gln	Thr	Val	Pro	Ile	Glu	Glu	Ala	35	40	45	
Gly	Ser	Met	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	50	55	60	
Pro	Leu	Leu	Leu	Leu	Lys	Leu	His	Leu	Trp	Pro	Gln	Leu	Arg	Trp	65	70	75	
Leu	Pro	Ala	Asp	Leu	Ala	Phe	Ala	Val	Arg	Ala	Leu	Cys	Cys	Lys	80	85	90	
Arg	Ala	Leu	Arg	Ala	Arg	Ala	Leu	Ala	Ala	Ala	Ala	Asp	Pro	95	100	105		
Glu	Gly	Pro	Glu	Gly	Gly	Cys	Ser	Leu	Ala	Trp	Arg	Leu	Ala	Glu	110	115	120	
Leu	Ala	Gln	Gln	Arg	Ala	Ala	His	Thr	Phe	Leu	Ile	His	Gly	Ser	125	130	135	
Arg	Arg	Phe	Ser	Tyr	Ser	Glu	Ala	Glu	Arg	Glu	Ser	Asn	Arg	Ala	140	145	150	
Ala	Arg	Ala	Phe	Leu	Arg	Ala	Leu	Gly	Trp	Asp	Trp	Gly	Pro	Asp	155	160	165	
Gly	Gly	Asp	Ser	Gly	Glu	Gly	Ser	Ala	Gly	Glu	Gly	Glu	Arg	Ala	170	175	180	
Ala	Pro	Gly	Ala	Gly	Asp	Ala	Ala	Ala	Gly	Ser	Gly	Ala	Glu	Phe	185	190	195	
Ala	Gly	Gly	Asp	Gly	Ala	Ala	Arg	Gly	Gly	Gly	Ala	Ala	Ala	Pro	200	205	210	

Leu Ser Pro Gly	Ala Thr Val Ala Leu	Leu Leu Pro Ala Gly	Pro
215		220	225
Glu Phe Leu Trp	Leu Trp Phe Gly Leu	Ala Lys Ala Gly Leu	Arg
230		235	240
Thr Ala Phe Val	Pro Thr Ala Leu Arg	Arg Gly Pro Leu Leu	His
245		250	255
Cys Leu Arg Ser	Cys Gly Ala Arg Ala	Leu Val Leu Ala Pro	Glu
260		265	270
Phe Leu Glu Ser	Leu Glu Pro Asp Leu	Pro Ala Leu Arg Ala	Met
275		280	285
Gly Leu His Leu	Trp Ala Ala Gly Pro	Gly Thr His Pro Ala	Gly
290		295	300
Ile Ser Asp Leu	Leu Ala Glu Val Ser	Ala Glu Val Asp Gly	Pro
305		310	315
Val Pro Gly Tyr	Leu Ser Ser Pro Gln	Ser Ile Thr Asp Thr	Cys
320		325	330
Leu Tyr Ile Phe	Thr Ser Gly Thr Thr	Gly Leu Pro Lys Ala	Ala
335		340	345
Arg Ile Ser His	Leu Lys Ile Leu Gln	Cys Gln Gly Phe Tyr	Gln
350		355	360
Leu Cys Gly Val	His Gln Glu Asp Val	Ile Tyr Leu Ala Leu	Pro
365		370	375
Leu Tyr His Met	Ser Gly Ser Leu Leu	Gly Ile Val Gly Cys	Met
380		385	390
Gly Ile Gly Ala	Thr Val Val Leu Lys	Ser Lys Phe Ser Ala	Gly
395		400	405
Gln Phe Trp Glu	Asp Cys Gln Gln His	Arg Val Thr Val Phe	Gln
410		415	420
Tyr Ile Gly Glu	Leu Cys Arg Tyr Leu	Val Asn Gln Pro Pro	Ser
425		430	435
Lys Ala Glu Arg	Gly His Lys Val Arg	Leu Ala Val Gly Ser	Gly
440		445	450
Leu Arg Pro Asp	Thr Trp Glu Arg Phe	Val Arg Arg Phe Gly	Pro
455		460	465
Leu Gln Val Leu	Glu Thr Tyr Gly Leu	Thr Glu Gly Asn Val	Ala
470		475	480
Thr Ile Asn Tyr	Thr Gly Gln Arg Gly	Ala Val Gly Arg Ala	Ser
485		490	495
Trp Leu Tyr Lys	His Ile Phe Pro Phe	Ser Leu Ile Arg Tyr	Asp

500	505	510
Val Thr Thr Gly Glu Pro Ile Arg Asp	Pro Gln Gly His Cys Met	
515	520	525
Ala Thr Ser Pro Gly Glu Pro Gly Leu	Leu Val Ala Pro Val Ser	
530	535	540
Gln Gln Ser Pro Phe Leu Gly Tyr Ala	Gly Gly Pro Glu Leu Ala	
545	550	555
Gln Gly Lys Leu Leu Lys Asp Val Phe	Arg Pro Gly Asp Val Phe	
560	565	570
Phe Asn Thr Gly Asp Leu Leu Val Cys	Asp Asp Gln Gly Phe Leu	
575	580	585
Arg Phe His Asp Arg Thr Gly Asp Thr	Phe Arg Trp Lys Gly Glu	
590	595	600
Asn Val Ala Thr Thr Glu Val Ala Glu	Val Phe Glu Ala Leu Asp	
605	610	615
Phe Leu Gln Glu Val Asn Val Tyr Gly	Val Thr Val Pro Gly His	
620	625	630
Glu Gly Arg Ala Gly Met Ala Ala Leu	Val Leu Arg Pro Pro His	
635	640	645
Ala Leu Asp Leu Met Gln Leu Tyr Thr	His Val Ser Glu Asn Leu	
650	655	660
Pro Pro Tyr Ala Arg Pro Arg Phe Leu	Arg Leu Gln Glu Ser Leu	
665	670	675
Ala Thr Thr Glu Thr Phe Lys Gln Gln	Lys Val Arg Met Ala Asn	
680	685	690
Glu Gly Phe Asp Pro Ser Thr Leu Ser	Asp Pro Leu Tyr Val Leu	
695	700	705
Asp Gln Ala Val Gly Ala Tyr Leu Pro	Leu Thr Thr Ala Arg Tyr	
710	715	720
Ser Ala Leu Leu Ala Gly Asn Leu Arg	Ile	
725	730	

<210> 103

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 103

gagagccatg gggctocacc tg 22

<210> 104
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 104
ggagaatgtg gccacaac 18

<210> 105
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 105
gccctggcac agtgactcca tagacg 26

<210> 106
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 106
atccacttca gcggacac 18

<210> 107
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 107
ccagtgccag gatacctctc ttccccccag agcataacag acacg 45

<210> 108
<211> 2579
<212> DNA
<213> Homo sapiens

<400> 108
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cctccacgca cacacatccc caagaacctc gagctcacac caacagacac 100
acgcgcgcat acacaactgc tctcgtttgt ccatctccct cccgggggag 150
ccggcgcgcg ctcccacott tgcgcacac tccggcgagc cgagcccgca 200

gcgctccagg attctgcggc tcggaactcg gattgcagct ctgaaccccc 250
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 accgtttcca tctgggggct agaggagcaa ggcagcagcc ttcccagcca 350
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 gcagtccaga gggctgcgct gctcgtcccc tcggctggca gaagggggtg 450
 acgctgggca gcggcgagga gcgcgccgct gcctctggcg ggctttcggc 500
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<210> 109

<211> 555

<212> PRT

<213> Homo sapiens

<400> 109

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Leu	Leu	Ser	Leu	Pro	Ala	Gly	Ala	Asp	Val	Lys	Ala	Arg	Ser	Cys
				20					25					30
Gly	Glu	Val	Arg	Gln	Ala	Tyr	Gly	Ala	Lys	Gly	Phe	Ser	Leu	Ala
				35					40					45
Asp	Ile	Pro	Tyr	Gln	Glu	Ile	Ala	Gly	Glu	His	Leu	Arg	Ile	Cys
				50					55					60
Pro	Gln	Glu	Tyr	Thr	Cys	Cys	Thr	Thr	Glu	Met	Glu	Asp	Lys	Leu
				65					70					75

Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr	80	85	90
Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	95	100	105
Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	110	115	120
Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn	125	130	135
Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr	140	145	150
Thr	Gly	Gly	Asn	Val	Asn	Leu	Glu	Glu	Met	Leu	Asn	Asp	Phe	Trp	155	160	165
Ala	Arg	Leu	Leu	Glu	Arg	Met	Phe	Gln	Leu	Ile	Asn	Pro	Gln	Tyr	170	175	180
His	Phe	Ser	Glu	Asp	Tyr	Leu	Glu	Cys	Val	Ser	Lys	Tyr	Thr	Asp	185	190	195
Gln	Leu	Lys	Pro	Phe	Gly	Asp	Val	Pro	Arg	Lys	Leu	Lys	Ile	Gln	200	205	210
Val	Thr	Arg	Ala	Phe	Ile	Ala	Ala	Arg	Thr	Phe	Val	Gln	Gly	Leu	215	220	225
Thr	Val	Gly	Arg	Glu	Val	Ala	Asn	Arg	Val	Ser	Lys	Val	Ser	Pro	230	235	240
Thr	Pro	Gly	Cys	Ile	Arg	Ala	Leu	Met	Lys	Met	Leu	Tyr	Cys	Pro	245	250	255
Tyr	Cys	Arg	Gly	Leu	Pro	Thr	Val	Arg	Pro	Cys	Asn	Asn	Tyr	Cys	260	265	270
Leu	Asn	Val	Met	Lys	Gly	Cys	Leu	Ala	Asn	Gln	Ala	Asp	Leu	Asp	275	280	285
Thr	Glu	Trp	Asn	Leu	Phe	Ile	Asp	Ala	Met	Leu	Leu	Val	Ala	Glu	290	295	300
Arg	Leu	Glu	Gly	Pro	Phe	Asn	Ile	Glu	Ser	Val	Met	Asp	Pro	Ile	305	310	315
Asp	Val	Lys	Ile	Ser	Glu	Ala	Ile	Met	Asn	Met	Gln	Glu	Asn	Ser	320	325	330
Met	Gln	Val	Ser	Ala	Lys	Val	Phe	Gln	Gly	Cys	Gly	Gln	Pro	Lys	335	340	345
Pro	Ala	Pro	Ala	Leu	Arg	Ser	Ala	Arg	Ser	Ala	Pro	Glu	Asn	Phe	350	355	360
Asn	Thr	Arg	Phe	Arg	Pro	Tyr	Asn	Pro	Glu	Glu	Arg	Pro	Thr	Thr			

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Met	Asn	Asp	Gly	Leu	Thr	Asn	Gln	Ile	Asn	Asn	Pro	Glu	Val	Asp
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Val	Asp	Ile	Thr	Arg	Pro	Asp	Thr	Phe	Ile	Arg	Gln	Gln	Ile	Met
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	485								490					495
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Ile Asn Ile Asn Arg Arg Arg Tyr Ala	Ala Met Leu Ser Cys Leu	
290	295	300
Asp Glu Ala Ile Asn Asn Val Thr Leu	Ala Leu Lys Thr Tyr Gly	
305	310	315
Phe Tyr Asn Asn Ser Ile Ile Ile Tyr	Ser Ser Asp Asn Gly Gly	
320	325	330
Gln Pro Thr Ala Gly Gly Ser Asn Trp	Pro Leu Arg Gly Ser Lys	
335	340	345
Gly Thr Tyr Trp Glu Gly Gly Ile Arg	Ala Val Gly Phe Val His	
350	355	360
Ser Pro Leu Leu Lys Asn Lys Gly Thr	Val Cys Lys Glu Leu Val	
365	370	375
His Ile Thr Asp Trp Tyr Pro Thr Leu	Ile Ser Leu Ala Glu Gly	
380	385	390
Gln Ile Asp Glu Asp Ile Gln Leu Asp	Gly Tyr Asp Ile Trp Glu	
395	400	405

Thr	Ile	Ser	Glu	Gly	Leu	Arg	Ser	Pro	Arg	Val	Asp	Ile	Leu	His
				410					415					420
Asn	Ile	Asp	Pro	Tyr	Thr	Pro	Arg	Gln	Lys	Met	Ala	Pro	Gly	Gln
				425					430					435
Gln	Ala	Met	Gly	Ser	Gly	Thr	Leu	Gln	Ser	Ser	Gln	Pro	Ser	Glu
				440					445					450
Cys	Ser	Thr	Gly	Asn	Cys	Leu	Gln	Glu	Ile	Leu	Ala	Thr	Ala	Thr
				455					460					465
Gly	Ser	Pro	Leu	Ser	Leu	Ser	Ala	Thr	Trp	Asp	Arg	Thr	Gly	Gly
				470					475					480
Thr	Met	Asn	Gly	Ser	Pro	Cys	Gln	Leu	Ala	Lys	Val	Tyr	Gly	Phe
				485					490					495
Ser	Thr	Ser	Gln	Pro	Thr	His	Met	Arg	Gly	Trp	Thr	Tyr	Leu	Thr
				500					505					510
Gly	Ile	Gln	Glu	Ser										
				515										

<210> 115
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 115
 cccaacccaa ctgtttacct ctgg 24

<210> 116
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 116
 ctctctgagt gtacatctgt gtgg 24

<210> 117
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<220>
 <221> unsure
 <222> 33
 <223> unknown base

<400> 117
gccaccctac ctcagaaaact gaaggagggtt ggntattcaa cgcatatggt 50
cgg 53

<210> 118
<211> 2260
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086
<223> unknown base

<400> 118
cggacgcgtg ggtgcgagtg gagcggagga cccgagcggc tgaggagaga 50
ggaggcggcg gcttagctgc tacgggggtcc ggccggcgcc ctcccagggg 100
gggctcagga ggaggaagga ggacccgtgc gagaatgcct ctgccctgga 150
gccttgcgct cccgctgctg ctctcctggg tggcagggtgg ttccgggaac 200
gcggccagtgc caaggcatca cgggttggtta gcatcggcac gtcagcctgg 250
ggtctgtcac tatggaacta aactggcctg ctgctacggc tggagaagaa 300
acagcaaggg agtctgtgaa gctacatgcg aacctggatg taagtttggt 350
gagtgcgtgg gaccaaaca atgcagatgc ttccaggat acaccgggaa 400
aacctgcagt caagatgtga atgagtgtgg aatgaaaccc cggccatgcc 450
aacacagatg tgtgaataca cacggaagct acaagtgctt ttgcctcagt 500
ggccacatgc tcatgccaga tgctacgtgt gtgaactcta ggacatgtgc 550
catgataaac tgtcagtaca gctgtgaaga cacagaagaa gggccacagt 600
gcctgtgtcc atcctcagga ctccgcctgg ccccaaattg aagagactgt 650
ctagatattg atgaatgtgc ctctggtaaa gtcattctgc cctacaatcg 700
aagatgtgtg aacacatttg gaagctacta ctgcaaattg cacattgggt 750
tcgaactgca atatatcagt ggacgatatg actgtataga tataaatgaa 800
tgtactatgg atagccatac gtgcagccac catgcccaatt gcttcaatac 850
ccaaggggtcc ttcaagtgtg aatgcaagca gggatataaa ggcaatggac 900
ttcgggtgtc tgctatccct gaaaattctg tgaaggaagt cctcagagca 950
cctggtacca tcaaagacag aatcaagaag ttgcttgctc aaaaaaacag 1000
catgaaaaag aaggcaaaaa ttaaaaatgt taccacagaa cccaccagga 1050

ctctacccc taaggtgaac ttgcagccct tcaactatga agagatagtt 1100
 tccagaggcg ggaactctca tggaggtaaa aaagggaatg aagagaaatg 1150
 aaagaggggc ttgaggatga gaaaagagaa gagaaagccc tgaagaatga 1200
 catagaggag cgaagcctgc gaggagatgt gtttttccct aaggtgaatg 1250
 aagcaggatga attcggcctg attctggtcc aaaggaaagc gctaacttcc 1300
 aaactggaac ataaagattt aaatatctcg gttgactgca gcttcaatca 1350
 tgggatctgt gactggaaac aggatagaga agatgatttt gactggaatc 1400
 ctgctgatcg agataatgct attggcttct atatggcagt tccggccttg 1450
 gcaggtcaca agaaagacat tggccgattg aaacttctcc tacctgacct 1500
 gcaaccccaa agcaacttct gtttgctctt tgattaccgg ctggccggag 1550
 acaaagtcgg gaaacttcga gtgtttgtga aaaacagtaa caatgccctg 1600
 gcatgggaga agaccacgag tgaggatgaa aagtggaaga cagggaat 1650
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 gtttcaggct tatgtccaga tagcctttta tctgtggatg actgaatggt 1800
 actatcttta tatttgactt tgtatgtcag ttccctgggt tttttgatat 1850
 tgcacatag gacctctggc attttagaat tactagctga aaaattgtaa 1900
 tgtaccaaca gaaatattat tgtaagatgc ctttcttgta taagatatgc 1950
 caatatttgc tttaaatatc atatcaactgt atcttctcag tcatttctga 2000
 atctttccnc attatattat aaaatntgga aangtcagtt tatctcccct 2050
 cctcngtata tctgatttgt atangtangt tgatgngctt ctctctacaa 2100
 catttctaga aaatagaaaa aaaagcacag agaaatgttt aactgtttga 2150
 ctcttatgat acttcttgga aactatgaca tcaaagatag acttttgcct 2200
 aagtggctta gctgggtctt tcatagccaa acttgtatat ttaattcttt 2250
 gtaataataa 2260

<210> 119
 <211> 338
 <212> PRT
 <213> Homo sapiens

<400> 119
 Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu Ser Trp
 1 5 10 15

Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	Gly		20	25	30
Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr		35	40	45
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val		50	55	60
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val		65	70	75
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr		80	85	90
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys		95	100	105
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys		110	115	120
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser		125	130	135
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr		140	145	150
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu		155	160	165
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser		170	175	180
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe		185	190	195
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr		200	205	210
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met		215	220	225
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln		230	235	240
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly		245	250	255
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu		260	265	270
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala		275	280	285
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr		290	295	300
Pro	Glu	Pro	Thr	Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro				

305

310

315

Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly
 320 325 330

Gly Lys Lys Gly Asn Glu Glu Lys
 335

<210> 120

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

cctcagtggc cacatgctca tg 22

<210> 121

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

ggctgcacgt atggctatcc atag 24

<210> 122

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

gataaactgt cagtacagct gtgaagacac agaagaaggg ccacagtgcc 50

<210> 123

<211> 1199

<212> DNA

<213> Homo sapiens

<400> 123

gggagctgct gctgtggctg ctggtgctgt gcgcgctgct cctgctcttg 50

gtgcagctgc tgcgcttcct gagggctgac ggcgacctga cgctactatg 100

ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatggtgg 150

tgtgggtgac tggagcctcg agtgggaattg gtgaggagct ggcttaccag 200

ttgtctaaac taggagtttc tcttgtgctg tcagccagaa gagtgcata 250

gctggaaagg gtgaaaagaa gatgcctaga gaatggcaat ttaaaagaaa 300

aagatataact tgttttggccc cttgacctga cgcacactgg ttcccatgaa 350
gcggctacca aagctgttct ccaggagttt ggtagaatcg acattctggt 400
caacaatggt ggaatgtccc agcgttctct gtgcatggat accagcttgg 450
atgtctacag aaagctaata gagcttaact acttagggac ggtgtccttg 500
acaaaatgtg ttctgcctca catgatcgag aggaagcaag gaaagattgt 550
tactgtgaat agcatcctgg gtatcatatc tgtacctctt tccattggat 600
actgtgctag caagcatgct ctccgggggtt tttttaatgg ccttcgaaca 650
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tgtgcaatca aatattgtgg agaattccct agctggagaa gtcacaaaga 750
ctataggcaa taatggagac cagtcccaca agatgacaac cagtcttgt 800
gtgcggctga tgttaatcag catggccaat gatttgaaag aagtttggat 850
ctcagaacaa cctttcttgt tagtaacata tttgtggcaa tacatgcaa 900
cctgggcctg gtggataacc aacaagatgg ggaagaaaag gattgagaac 950
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aaaacatgac tgaaaagagc acctgtactt ttcaagccac tggagggaga 1050
aatggaaaac atgaaaacag caatcttctt atgcttctga ataataaag 1100
actaatttgt gattttactt tttaatagat atgactttgc ttccaacatg 1150
gaatgaaata aaaaataaat aataaaagat tgccatgaat cttgcaaaa 1199

<210> 124
<211> 289
<212> PRT
<213> Homo sapiens

<400> 124
Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu Glu
1 5 10 15
Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser
20 25 30
Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu
35 40 45
Glu Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu
50 55 60
Asp Leu Thr Asp Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val
65 70 75
Leu Gln Glu Phe Gly Arg Ile Asp Ile Leu Val Asn Asn Gly Gly

80										85					90				
Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr					
				95					100					105					
Arg	Lys	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr					
				110					115					120					
Lys	Cys	Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile					
				125					130					135					
Val	Thr	Val	Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser					
				140					145					150					
Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	Ala	Leu	Arg	Gly	Phe	Phe	Asn					
				155					160					165					
Gly	Leu	Arg	Thr	Glu	Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser					
				170					175					180					
Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	Ile	Val	Glu	Asn	Ser					
				185					190					195					
Leu	Ala	Gly	Glu	Val	Thr	Lys	Thr	Ile	Gly	Asn	Asn	Gly	Asp	Gln					
				200					205					210					
Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile					
				215					220					225					
Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro					
				230					235					240					
Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala					
				245					250					255					
Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe					
				260					265					270					
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys					
				275					280					285					

Thr Lys His Asp

<210> 125
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 125
 gcaatgaact gggagctgc 19

 <210> 126
 <211> 19
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

cttttcaagc cactggaggg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgtagacat ccaagctggt atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

aagagtctgc atccacacca ctc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatggggc gagtggcagg gacgacgccc agaattg 46

<210> 131

<211> 2365

<212> DNA

<213> Homo sapiens

<400> 131

gcgacgtggg caccgccatc agctgttgcg gcgtcttctc ctccaggtgg 50
 ggcagggggtt tcgggctggg ggagcatgtg ctgggacagg acagcatcct 100
 caatcaatcc aacagcatat tcgggttgcg cttctacaca ctacagctat 150
 tgtaggttg cctgcggaca cgctgggcct ctgtcctgat gctgctgagc 200
 tccctgggtg ctctcgctgg ttctgtctac ctggcctgga tcctgttctt 250
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 gctaagagggc actgagccct caaccaagc caggctgacc tcctctgctt 400
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 ccccccaag cctcaggagg gcaacacagt ccctggcgag tggccctggc 500
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 agggagacgc tcctgtgctg ctgaccaaca cagctgctca cagttcctgg 1150
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 ggcggtgcta actgctgccc actgcttcat tgggcgccag gccccagagg 1400
 aatggagcgt agggctgggg accagaccgg aggagtgggg cctgaagcag 1450

ctcactctgc atggagccta caccaccct gaggggggct acgacatggc 1500
 cctcctgctg ctggcccagc ctgtgacact gggagccagc ctgcggcccc 1550
 tctgcctgcc ctatcctgac caccacctgc ctgatgggga gcgtggctgg 1600
 gttctgggac gggcccgcgc aggagcaggc atcagctccc tccagacagt 1650
 gcccgtagcc ctctggggc ctagggcctg cagccggctg catgcagctc 1700
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 agagcccag gctgagcctg gaagctgcct ggccaacata agccaaccaa 2000
 ccagctgctg acaggggacc tggccattct caggacaaga gaatgcaggc 2050
 aggcaaattg cattactgcc cctgtcctcc ccaccctgtc atgtgtgatt 2100
 ccaggcacca gggcaggccc agaagcccag cagctgtggg aaggaacctg 2150
 cctggggcca caggtgcccc cccccaccc tgcaggacag ggggtgtctgt 2200
 ggacactccc acacccaact ctgtaccac gaggcgtct cagctttcct 2250
 cctcctttac tctttcagat acaatcacgc cagccacgtt gttttgaaaa 2300
 tttctttttt tggggggcag cagttttcct ttttttaaac ttaaataaat 2350
 tgttacaaaa taaaa 2365

<210> 132

<211> 571

<212> PRT

<213> Homo sapiens

<400> 132

Met	Leu	Leu	Ser	Ser	Leu	Val	Ser	Leu	Ala	Gly	Ser	Val	Tyr	Leu
1				5					10					15

Ala	Trp	Ile	Leu	Phe	Phe	Val	Leu	Tyr	Asp	Phe	Cys	Ile	Val	Cys
			20						25					30

Ile	Thr	Thr	Tyr	Ala	Ile	Asn	Val	Ser	Leu	Met	Trp	Leu	Ser	Phe
			35						40					45

Arg	Lys	Val	Gln	Glu	Pro	Gln	Gly	Lys	Ala	Lys	Arg	His	Gly	Asn
			50						55					60

Thr	Val	Pro	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Val	Arg	Arg	Gln
			65						70					75

Gly	Ala	His	Ile	Cys	Ser	Gly	Ser	Leu	Val	Ala	Asp	Thr	Trp	Val	80	85	90
Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Lys	Ala	Ala	Ala	Thr	Glu	Leu	95	100	105
Asn	Ser	Trp	Ser	Val	Val	Leu	Gly	Ser	Leu	Gln	Arg	Glu	Gly	Leu	110	115	120
Ser	Pro	Gly	Ala	Glu	Glu	Val	Gly	Val	Ala	Ala	Leu	Gln	Leu	Pro	125	130	135
Arg	Ala	Tyr	Asn	His	Tyr	Ser	Gln	Gly	Ser	Asp	Leu	Ala	Leu	Leu	140	145	150
Gln	Leu	Ala	His	Pro	Thr	Thr	His	Thr	Pro	Leu	Cys	Leu	Pro	Gln	155	160	165
Pro	Ala	His	Arg	Phe	Pro	Phe	Gly	Ala	Ser	Cys	Trp	Ala	Thr	Gly	170	175	180
Trp	Asp	Gln	Asp	Thr	Ser	Asp	Ala	Pro	Gly	Thr	Leu	Arg	Asn	Leu	185	190	195
Arg	Leu	Arg	Leu	Ile	Ser	Arg	Pro	Thr	Cys	Asn	Cys	Ile	Tyr	Asn	200	205	210
Gln	Leu	His	Gln	Arg	His	Leu	Ser	Asn	Pro	Ala	Arg	Pro	Gly	Met	215	220	225
Leu	Cys	Gly	Gly	Pro	Gln	Pro	Gly	Val	Gln	Gly	Pro	Cys	Gln	Gly	230	235	240
Asp	Ser	Gly	Gly	Pro	Val	Leu	Cys	Leu	Glu	Pro	Asp	Gly	His	Trp	245	250	255
Val	Gln	Ala	Gly	Ile	Ile	Ser	Phe	Ala	Ser	Ser	Cys	Ala	Gln	Glu	260	265	270
Asp	Ala	Pro	Val	Leu	Leu	Thr	Asn	Thr	Ala	Ala	His	Ser	Ser	Trp	275	280	285
Leu	Gln	Ala	Arg	Val	Gln	Gly	Ala	Ala	Phe	Leu	Ala	Gln	Ser	Pro	290	295	300
Glu	Thr	Pro	Glu	Met	Ser	Asp	Glu	Asp	Ser	Cys	Val	Ala	Cys	Gly	305	310	315
Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp	320	325	330
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly	335	340	345
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys	350	355	360
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly			

	365	370	375
Thr Arg Pro Glu	Glu Trp Gly Leu Lys	Gln Leu Ile Leu His	Gly
	380	385	390
Ala Tyr Thr His	Pro Glu Gly Gly Tyr	Asp Met Ala Leu Leu	Leu
	395	400	405
Leu Ala Gln Pro	Val Thr Leu Gly Ala	Ser Leu Arg Pro Leu	Cys
	410	415	420
Leu Pro Tyr Pro	Asp His His Leu Pro	Asp Gly Glu Arg Gly	Trp
	425	430	435
Val Leu Gly Arg	Ala Arg Pro Gly Ala	Gly Ile Ser Ser Leu	Gln
	440	445	450
Thr Val Pro Val	Thr Leu Leu Gly Pro	Arg Ala Cys Ser Arg	Leu
	455	460	465
His Ala Ala Pro	Gly Gly Asp Gly Ser	Pro Ile Leu Pro Gly	Met
	470	475	480
Val Cys Thr Ser	Ala Val Gly Glu Leu	Pro Ser Cys Glu Gly	Leu
	485	490	495
Ser Gly Ala Pro	Leu Val His Glu Val	Arg Gly Thr Trp Phe	Leu
	500	505	510
Ala Gly Leu His	Ser Phe Gly Asp Ala	Cys Gln Gly Pro Ala	Arg
	515	520	525
Pro Ala Val Phe	Thr Ala Leu Pro Ala	Tyr Glu Asp Trp Val	Ser
	530	535	540
Ser Leu Asp Trp	Gln Val Tyr Phe Ala	Glu Glu Pro Glu Pro	Glu
	545	550	555
Ala Glu Pro Gly	Ser Cys Leu Ala Asn	Ile Ser Gln Pro Thr	Ser
	560	565	570

Cys

<210> 133

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

cctgtgctgt gcctcgagcc tgac 24

<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gtttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

cgggccgccc cgggccccca ttcgggccgg gcctcgctgc ggcggcgact 50

gagccaggct gggccgcgtc cctgagtcct agagtcggcg cggcgcggca 100

ggggcagcct tccaccacgg ggagcccagc tgtcagccgc ctcacaggaa 150

gatgctgcgt cggcggggca gccctggcat ggggtgtcat gtgggtgcag 200

ccctgggagc actgtggttc tgcctcacag gagccctgga ggtccaggtc 250

cctgaagacc cagtgggtggc actggtgggc accgatgcca ccctgtgctg 300

ctccttctcc cctgagcctg gcttcagcct ggcacagctc aacctcatct 350

ggcagctgac agatacaaaa cagctgggtgc acagctttgc tgagggccag 400

gaccagggca ggcctatgc caaccgcacg gccctcttcc cggacctgct 450

ggcacagggc aacgcatccc tgaggctgca ggcgtgctgt gtggcggacg 500

agggcagctt cacctgcttc gtgagcatcc gggatttcgg cagcgtgcc 550

gtcagcctgc aggtggccgc tccctactcg aagcccagca tgaccctgga 600

gccaacaag gacctgcggc caggggacac ggtgaccatc acgtgctcca 650

gctaccaggg ctaccctgag gctgaggtgt tctggcagga tgggcagggt 700

gtgcccctga ctggcaacgt gaccacgtcg cagatggcca acgagcaggg 750

cttgtttgat gtgcacagcg tccctgcgggt ggtgctgggt gcgaatggca 800

cctacagctg cctgggtgcg aaccccgctg tgcagcagga tgcgcacrgc 850

tctgtcacca tcacagggca gcctatgaca ttccccccag aggccctgtg 900
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 ctttcgtgtg ctggagaaaag atcaaacaga gctgtgagga ggagaatgca 1000
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 gaccatgagg accagggagc tgctaccctt ccctacagct cctaccctct 1150
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 ttttcttata gacacaatga acagaccacc cacaacctta gttctctaag 1350
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 ctgccttatt tcaccaaaga cagcatgcat agtcaccccg gccttgtttc 1550
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 catagaatct tttcttctca gacagggaca gtgcggcctc aacatctcct 1650
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 gcctctggcc agctcctggc ctctggtaga gtgagacttc agacgttctg 1850
 atgccttccg gatgtcatct ctccctgccc caggaatgga agatgtgagg 1900
 acttctaatt taaatgtggg actcggaggg attttgtaaa ctgggggtat 1950
 attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

Met Leu Arg Arg Arg Gly Ser Pro Gly Met Gly Val His Val Gly

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20		25	30
Val Gln Val Pro	Glu Asp Pro Val Val	Ala Leu Val Gly Thr	Asp
35		40	45
Ala Thr Leu Cys Cys	Ser Phe Ser Pro	Glu Pro Gly Phe Ser	Leu
50		55	60
Ala Gln Leu Asn Leu	Ile Trp Gln Leu Thr	Asp Thr Lys Gln Leu	
65		70	75
Val His Ser Phe Ala	Glu Gly Gln Asp	Gln Gly Ser Ala Tyr	Ala
80		85	90
Asn Arg Thr Ala Leu	Phe Pro Asp Leu Leu	Ala Gln Gly Asn Ala	
95		100	105
Ser Leu Arg Leu Gln	Arg Val Arg Val	Ala Asp Glu Gly Ser	Phe
110		115	120
Thr Cys Phe Val Ser	Ile Arg Asp Phe	Gly Ser Ala Ala Val	Ser
125		130	135
Leu Gln Val Ala Ala	Pro Tyr Ser Lys	Pro Ser Met Thr Leu	Glu
140		145	150
Pro Asn Lys Asp Leu	Arg Pro Gly Asp	Thr Val Thr Ile Thr	Cys
155		160	165
Ser Ser Tyr Gln Gly	Tyr Pro Glu Ala	Glu Val Phe Trp Gln	Asp
170		175	180
Gly Gln Gly Val Pro	Leu Thr Gly Asn	Val Thr Thr Ser Gln	Met
185		190	195
Ala Asn Glu Gln Gly	Leu Phe Asp Val	His Ser Val Leu Arg	Val
200		205	210
Val Leu Gly Ala Asn	Gly Thr Tyr Ser	Cys Leu Val Arg Asn	Pro
215		220	225
Val Leu Gln Gln Asp	Ala His Xaa Ser	Val Thr Ile Thr Gly	Gln
230		235	240
Pro Met Thr Phe Pro	Pro Glu Ala Leu	Trp Val Thr Val Gly	Leu
245		250	255
Ser Val Cys Leu Ile	Ala Leu Leu Val	Ala Leu Ala Phe Val	Cys
260		265	270
Trp Arg Lys Ile Lys	Gln Ser Cys Glu	Glu Glu Asn Ala Gly	Ala
275		280	285
Glu Asp Gln Asp Gly	Glu Gly Glu Gly	Ser Lys Thr Ala Leu	Gln
290		295	300

Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile
 305 310 315

Ala

<210> 138
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 138
 ctggcacagc tcaacctcat ctgg 24

<210> 139
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 139
 gctgtctgtc tgtctcattg 20

<210> 140
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 140
 ggacacagta tactgaccac 20

<210> 141
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 141
 tgccaaccag gcagctgtaa gtgc 24

<210> 142
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 142
tggaagaaga ggggtggtgat gtgg 24

<210> 143

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 143

cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144

<211> 2336

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1620, 1673

<223> unknown base

<400> 144

ttcgtgaccc ttgagaaaag agttggtggt aaatgtgcca cgtcttctaa 50

gaagggggag tcctgaactt gtctgaagcc cttgtccgta agccttgaac 100

tacgttctta aatctatgaa gtcgaggac ctttcgctgc tttttagagg 150

acttctttcc ttgcttcagc aacatgaggc ttttcttgtg gaacgcggtc 200

ttgactctgt tcgtcacttc tttgattggg gctttgatcc ctgaaccaga 250

agtgaaaatt gaagttctcc agaagccatt catctgccat cgcaagacca 300

aaggagggga tttgatgttg gtccactatg aaggctaact agaaaaggac 350

ggctccttat ttcactccac tcacaaacat aacaatgggc agcccatttg 400

gtttaccctg ggcacccctg aggctctcaa aggttgggac cagggttga 450

aaggaatgtg tgtaggagag aagagaaagc tcatcattcc tcctgctctg 500

ggctatggaa aagaaggaaa aggtaaaatt cccccagaaa gtacactgat 550

atttaatat gatctcctgg agattcgaaa tggaccaaga tcccatgaat 600

cattccaaga aatggatctt aatgatgact ggaaactctc taaagatgag 650

gttaaagcat atttaaagaa ggagtttgaa aaacatgggtg cggtggtgaa 700

tgaaagtcac catgatgctt tgggtggagga tatttttgat aaagaagatg 750

aagacaaaga tgggtttata tctgccagag aatttacata taaacacgat 800

gagttataga gatacatcta cccttttaac atagcactca tctttcaaga 850

gcagctacta ttgaataaat acctatcctg gatttt 2336

<210> 145

<211> 211

<212> PRT

<213> Homo sapiens

<400> 145

Met Arg Leu Phe Leu Trp Asn Ala Val Leu Thr Leu Phe Val Thr
1 5 10 15

Ser Leu Ile Gly Ala Leu Ile Pro Glu Pro Glu Val Lys Ile Glu
20 25 30

Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly
35 40 45

Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly
50 55 60

Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro Ile
65 70 75

Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln
80 85 90

Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu Ile Ile
95 100 105

Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro
110 115 120

Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg
125 130 135

Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn
140 145 150

Asp Asp Trp Lys Leu Ser Lys Asp Glu Val Lys Ala Tyr Leu Lys
155 160 165

Lys Glu Phe Glu Lys His Gly Ala Val Val Asn Glu Ser His His
170 175 180

Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp Glu Asp Lys
185 190 195

Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His Asp Glu
200 205 210

Leu

<210> 146

<211> 26

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 146
ctttccttgc ttcagcaaca tgaggc 26

<210> 147
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 147
gcccagagca ggaggaatga tgagc 25

<210> 148
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 148
gtggaacgcg gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<210> 149
<211> 2196
<212> DNA
<213> Homo sapiens

<400> 149
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tttttttagc atccaaccat tcttcccttg tagttctcgc cccctcaaatt 100
caccctctcc cgtagccac ccgactaaca tctcagtctc tgaaaatgca 150
cagagatgcc tggctacctc gccctgcctt cagcctcacg gggctcagtc 200
tctttttctc tttggtgcc aaggagcgga gcatggaggt cacagtacct 250
gccaccctca acgtcctcaa tggctctgac gccgcctgc cctgcacctt 300
caactcctgc tacacagtga accacaaaca gttctccctg aactggactt 350
accaggagtg caacaactgc tctgaggaga tgttctcca gttccgcatg 400
aagatcatta acctgaagct ggagcgggtt caagaccgcg tggagttctc 450
agggaacccc agcaagtacg atgtgtcggg gatgctgaga aacgtgcagc 500
cggaggatga ggggatttac aactgctaca tcatgaaccc cctgaccgc 550
cacctgggcc atggcaagat ccatctgcag gtcctcatgg aagagcccc 600

tgagcgggac tccacggtgg ccgtgattgt gggcgcctcc gtcgggggct 650
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 aaaaaagagc agaagctgag cacagatgac ctgaagaccg aggaggagg 750
 caagacggac ggtgaaggca acccgatga tggcgccaag tagtgggtgg 800
 cggccctgc agcctcccg gtcccgcttc ctcctcttc cgcctgtac 850
 agtgaccctg cctgctcgct cttggtgtgc ttcctgtgac ctaggacccc 900
 agggcccacc tggggcctcc tgaacccccg acttcgtatc tcccaccctg 950
 caccaagagt gaccactct cttccatccg agaaacctgc catgctctgg 1000
 gacgtgtggg ccctggggag aggagagaaa gggcctccac ctgccagtcc 1050
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 ggcagtggct tcagagagga cctggtgggg agggagggct ttcctgtgct 1200
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 ataaggggag gccttggaac ctgagctgcc aatgccagcc ctgtcccatc 1850
 tgcggccacg ctactcgctc ctctcccaac aactcccttc gtggggacaa 1900
 aagtgacaat tgtaggccag gcacagtggc tcacgcctgt aatcccagca 1950
 ctttgaggag ccaaggcggg tggattacct ccactgttt agtagaaatg 2000
 ggcaaaaccc catctctact aaaaatacaa gaattagctg ggcgtggtgg 2050

cgtgtgcctg taatcccagc tatttgggag gctgaggcag gagaatcgct 2100
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 tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaa 2196

<210> 150
 <211> 215
 <212> PRT
 <213> Homo sapiens

<400> 150

Met	His	Arg	Asp	Ala	Trp	Leu	Pro	Arg	Pro	Ala	Phe	Ser	Leu	Thr	1	5	10	15
Gly	Leu	Ser	Leu	Phe	Phe	Ser	Leu	Val	Pro	Pro	Gly	Arg	Ser	Met	20	25	30	
Glu	Val	Thr	Val	Pro	Ala	Thr	Leu	Asn	Val	Leu	Asn	Gly	Ser	Asp	35	40	45	
Ala	Arg	Leu	Pro	Cys	Thr	Phe	Asn	Ser	Cys	Tyr	Thr	Val	Asn	His	50	55	60	
Lys	Gln	Phe	Ser	Leu	Asn	Trp	Thr	Tyr	Gln	Glu	Cys	Asn	Asn	Cys	65	70	75	
Ser	Glu	Glu	Met	Phe	Leu	Gln	Phe	Arg	Met	Lys	Ile	Ile	Asn	Leu	80	85	90	
Lys	Leu	Glu	Arg	Phe	Gln	Asp	Arg	Val	Glu	Phe	Ser	Gly	Asn	Pro	95	100	105	
Ser	Lys	Tyr	Asp	Val	Ser	Val	Met	Leu	Arg	Asn	Val	Gln	Pro	Glu	110	115	120	
Asp	Glu	Gly	Ile	Tyr	Asn	Cys	Tyr	Ile	Met	Asn	Pro	Pro	Asp	Arg	125	130	135	
His	Arg	Gly	His	Gly	Lys	Ile	His	Leu	Gln	Val	Leu	Met	Glu	Glu	140	145	150	
Pro	Pro	Glu	Arg	Asp	Ser	Thr	Val	Ala	Val	Ile	Val	Gly	Ala	Ser	155	160	165	
Val	Gly	Gly	Phe	Leu	Ala	Val	Val	Ile	Leu	Val	Leu	Met	Val	Val	170	175	180	
Lys	Cys	Val	Arg	Arg	Lys	Lys	Glu	Gln	Lys	Leu	Ser	Thr	Asp	Asp	185	190	195	
Leu	Lys	Thr	Glu	Glu	Glu	Gly	Lys	Thr	Asp	Gly	Glu	Gly	Asn	Pro	200	205	210	
Asp	Asp	Gly	Ala	Lys	215													

<210> 151

<211> 524
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 103, 233
<223> unknown base

<400> 151
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tcttcccttg tagttctcgc cccctcaaat caccttctcc cttagcccac 100
ccnactaaca tctcagtctc tgaaaatgca cagagatgcc tggctacctc 150
gccctgcctt cagcctcacg gggctcagtc tctttttctc tttggtgcca 200
ccaggacgga gcatggaggt ccacagtacc tgnccaccct caacgtcctc 250
aatggctctg acgcccgcct gccctgccct tcaactcctg ctacacagtg 300
aaccacaaac agttctccct gaactggact taccaggagt gcaacaactg 350
ctctgaggag atgttctctc agttccgcat gaagatcatt aacctgaagc 400
tggagcggtt tcaagaccgc gtggagtctc cagggaaacc cagcaagtac 450
gatgtgtcgg tgatgctgag aaacgtgcag ccggaggatg aggggattta 500
caactgctac atcatgaacc cccc 524

<210> 152
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 56, 123
<223> unknown base

<400> 152
tcacggggct catctctttt tctcttttgt gccaccagg acggagcatg 50
gaggtncaca tacctgccac cctcaacgtc ctcaatggtt ttgacgcccg 100
cctgccctgc accttcaact ccngctacac agtgaaccac aaacagttct 150
ccctgaactg gatttaccag gagtgaaca actggctctg aggagatgtt 200
cctccagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcggtt 250
ttcaagaacc gcgtggaagt ttctcaggga accccagcaa gtacgatgtg 300
tcggtgatgc tgagaaacgt gcagccggag gatgagggga tttacaactg 350
ctacatcatg aaccccc 368

<210> 153
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 153
acggagcatg gaggtccaca gtac 24

<210> 154
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 154
gcacgtttct cagcatcacc gac 23

<210> 155
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 155
cgccctgccct gcaccttcaa ctctgtctac acagtgaacc acaaacagtt 50

<210> 156
<211> 2680
<212> DNA
<213> Homo sapiens

<400> 156
tgcggcgacc gtcgtacacc atgggcctcc acctccgccc ctaccgtgtg 50
gggctgctcc cggatggcct cctgttcctc ttgtgtgtgc taatgtgtgt 100
cgcggaacca gcgctccgg ccggacgtca cccccagtg gtgctgggtcc 150
ctggtgattt gggtaaccaa ctggaagcca agctggacaa gcgacagtg 200
gtgcactacc tctgtccaa gaagaccgaa agctacttca caatctggct 250
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gttgcgttct tcgtggttcc caggccctgg gacatctcac tccactccta 1900
cctcccttac caccaggagc attcaagctc tggattgggc agcagatgtg 1950

cccccagttcc cgcaggtgtgt gttccagggg ccctgatttc ctcggtatgtg 2000
 ctattggccc caggactgaa gctgcctccc ttcaccctgg gactgtgggtt 2050
 ccaaggatga gagcaggggt tggagccatg gccttctggg aacctatgga 2100
 gaaaggggaat ccaaggaagc agccaaggct gctcgcagct tccctgagct 2150
 gcacctcttg ctaaccccac catcacactg ccaccctgcc ctagggtctc 2200
 actagtacca agtgggtcag cacagggctg aggatggggc tcctatccac 2250
 cctggccagc acccagctta gtgctgggac tagcccagaa acttgaatgg 2300
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 ctgccccagg gtgctccatg gatctccctg tggcagcagg catggagagt 2400
 cagggctgcc ttcattggcag taggctctaa gtgggtgact ggccacaggc 2450
 cgagaaaagg gtacagcctc taggtggggg tcccaaagac gccttcaggc 2500
 tggactgagc tgctctccca cagggtttct gtgcagctgg attttctctg 2550
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 atgtgtataa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157

<211> 412

<212> PRT

<213> Artificial

<400> 157

Met	Gly	Leu	His	Leu	Arg	Pro	Tyr	Arg	Val	Gly	Leu	Leu	Pro	Asp
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Gly	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Leu	Ala	Asp	Pro
				20					25					30
Ala	Leu	Pro	Ala	Gly	Arg	His	Pro	Pro	Val	Val	Leu	Val	Pro	Gly
				35					40					45
Asp	Leu	Gly	Asn	Gln	Leu	Glu	Ala	Lys	Leu	Asp	Lys	Pro	Thr	Val
				50					55					60
Val	His	Tyr	Leu	Cys	Ser	Lys	Lys	Thr	Glu	Ser	Tyr	Phe	Thr	Ile
				65					70					75
Trp	Leu	Asn	Leu	Glu	Leu	Leu	Leu	Pro	Val	Ile	Ile	Asp	Cys	Trp
				80					85					90
Ile	Asp	Asn	Ile	Arg	Leu	Val	Tyr	Asn	Lys	Thr	Ser	Arg	Ala	Thr
				95					100					105
Gln	Phe	Pro	Asp	Gly	Val	Asp	Val	Arg	Val	Pro	Gly	Phe	Gly	Lys

Thr	Phe	Ser	Leu	Glu	Phe	Leu	Asp	Pro	Ser	Lys	Ser	Ser	Val	Gly
				125					130					135
Ser	Tyr	Phe	His	Thr	Met	Val	Glu	Ser	Leu	Val	Gly	Trp	Gly	Tyr
				140					145					150
Thr	Arg	Gly	Glu	Asp	Val	Arg	Gly	Ala	Pro	Tyr	Asp	Trp	Arg	Arg
				155					160					165
Ala	Pro	Asn	Glu	Asn	Gly	Pro	Tyr	Phe	Leu	Ala	Leu	Arg	Glu	Met
				170					175					180
Ile	Glu	Glu	Met	Tyr	Gln	Leu	Tyr	Gly	Gly	Pro	Val	Val	Leu	Val
				185					190					195
Ala	His	Ser	Met	Gly	Asn	Met	Tyr	Thr	Leu	Tyr	Phe	Leu	Gln	Arg
				200					205					210
Gln	Pro	Gln	Ala	Trp	Lys	Asp	Lys	Tyr	Ile	Arg	Ala	Phe	Val	Ser
				215					220					225
Leu	Gly	Ala	Pro	Trp	Gly	Gly	Val	Ala	Lys	Thr	Leu	Arg	Val	Leu
				230					235					240
Ala	Ser	Gly	Asp	Asn	Asn	Arg	Ile	Pro	Val	Ile	Gly	Pro	Leu	Lys
				245					250					255
Ile	Arg	Glu	Gln	Gln	Arg	Ser	Ala	Val	Ser	Thr	Ser	Trp	Leu	Leu
				260					265					270
Pro	Tyr	Asn	Tyr	Thr	Trp	Ser	Pro	Glu	Lys	Val	Phe	Val	Gln	Thr
				275					280					285
Pro	Thr	Ile	Asn	Tyr	Thr	Leu	Arg	Asp	Tyr	Arg	Lys	Phe	Phe	Gln
				290					295					300
Asp	Ile	Gly	Phe	Glu	Asp	Gly	Trp	Leu	Met	Arg	Gln	Asp	Thr	Glu
				305					310					315
Gly	Leu	Val	Glu	Ala	Thr	Met	Pro	Pro	Gly	Val	Gln	Leu	His	Cys
				320					325					330
Leu	Tyr	Gly	Thr	Gly	Val	Pro	Thr	Pro	Asp	Ser	Phe	Tyr	Tyr	Glu
				335					340					345
Ser	Phe	Pro	Asp	Arg	Asp	Pro	Lys	Ile	Cys	Phe	Gly	Asp	Gly	Asp
				350					355					360
Gly	Thr	Val	Asn	Leu	Lys	Ser	Ala	Leu	Gln	Cys	Gln	Ala	Trp	Gln
				365					370					375
Ser	Arg	Gln	Glu	His	Gln	Val	Leu	Leu	Gln	Glu	Leu	Pro	Gly	Ser
				380					385					390
Glu	His	Ile	Glu	Met	Leu	Ala	Asn	Ala	Thr	Thr	Leu	Ala	Tyr	Leu
				395					400					405

Lys Arg Val Leu Leu Gly Pro
410

<210> 158

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 158

ctggggctac acacggggtg agg 23

<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 159

ggtgccgctg cagaaagtag agcg 24

<210> 160

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 160

gccccaaatg aaaacggggc ctacttcctg gccctccgcg agatg 45

<210> 161

<211> 1512

<212> DNA

<213> Homo sapiens

<400> 161

cggacgcgtg ggcggacgcg tggggcggcg gcagcggcgg cgacggcgac 50

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gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150

tcttcgcctt gatcgtgttc tcttgcattc atggtgaggg ctacagcaat 200

gccacgagt ctaagcagat gtactgcgtg ttcaaccgca acgaggatgc 250

ctgccgctat ggcagtgcc tgggggtgct ggccttcctg gcctcggcct 300

tcttcttggg ggtcgacgcg tatttcccc agatcagcaa cgccactgac 350

cgcaagtacc tggtcattgg tgacctgctc ttctcagctc tctggacctt 400

cctgtgggttt gttgggtttct gcttcctcac caaccagtgg gcagtcacca 450
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gacaactacc aacagccacc cttcaccag aacgcggaga ccaccgaggg 700
ctaccagcog cccctgtgt actgagtggc ggtagcgtg ggaaggggga 750
cagagagggc cctccctctt gccctggact ttcccatcag cctcctggaa 800
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gtgccccatg gctcccagac tctgtctgtg ccgagtgtat tataaaatcg 1450
tgggggagat gcccggcctg ggatgctgtt tggagacgga ataaatgttt 1500
tctcattcaa ag 1512

<210> 162

<211> 224

<212> PRT

<213> Homo sapiens

<400> 162

Met	Glu	Ser	Gly	Ala	Tyr	Gly	Ala	Ala	Lys	Ala	Gly	Gly	Ser	Phe
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Asp	Leu	Arg	Arg	Phe	Leu	Thr	Gln	Pro	Gln	Val	Val	Ala	Arg	Ala
				20					25					30

Val	Cys	Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly	
				35					40					45	
Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val	
				50					55					60	
Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly	
				65					70					75	
Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala	
				80					85					90	
Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val	
				95					100					105	
Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe	
				110					115					120	
Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro	
				125					130					135	
Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr	
				140					145					150	
Phe	Ser	Phe	Phe	Ser	Ile	Phe	Ser	Trp	Gly	Val	Leu	Ala	Ser	Leu	
				155					160					165	
Ala	Tyr	Gln	Arg	Tyr	Lys	Ala	Gly	Val	Asp	Asp	Phe	Ile	Gln	Asn	
				170					175					180	
Tyr	Val	Asp	Pro	Thr	Pro	Asp	Pro	Asn	Thr	Ala	Tyr	Ala	Ser	Tyr	
				185					190					195	
Pro	Gly	Ala	Ser	Val	Asp	Asn	Tyr	Gln	Gln	Pro	Pro	Phe	Thr	Gln	
				200					205					210	
Asn	Ala	Glu	Thr	Thr	Glu	Gly	Tyr	Gln	Pro	Pro	Pro	Val	Tyr		
				215					220						

<210> 163

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

tggtcttcgc cttgatcgtg ttct 24

<210> 164

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164
gtgtactgag cggcggttag 20

<210> 165
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 165
ctgaaggtga tggctgccct cac 23

<210> 166
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

CCAGGAGGCT CATGGGAAAG TCC 23
<400> 166

<210> 167
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

CCACGAGTCT AAGCAGATGT ACTGCGTGTT CAACCGCAAC GAGGATGCCT 50
<400> 167

<210> 168
<211> 3143
<212> DNA
<213> Homo sapiens

<400> 168
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agggtgatca gtgagcagaa ggatgcccggt ggccgaggcc cccaggtgg 100
ctggcgggca gggggacgga ggtgatggcg aggaagcgga gccagagggg 150
atgttcaagg cctgtgagga ctccaagaga aaagcccggg gctacctccg 200
cctggtgccc ctgtttgtgc tgctggccct gctcgtgctg gcttcggcgg 250
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caggtgtact caggcagtct gcgtgtactc aatcgccact tctcccagga 350
tcttaccgcg cggaatcta gtgccttccg cagtgaacc gccaaagccc 400

agaagatgct caaggagctc atcaccagca cccgcctggg aacttactac 450
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ctggttcatt ctccaaatcc ccgagcaccg ccggctgatg ctgagccccg 550
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tttgaataa agctgcctga tcaaaaaaaaa aaaaaaaaaa aaa 3143

<210> 169
<211> 802
<212> PRT
<213> Homo sapiens
<400> 169

Met	Pro	Val	Ala	Glu	Ala	Pro	Gln	Val	Ala	Gly	Gly	Gln	Gly	Asp	1	5	10	15
Gly	Gly	Asp	Gly	Glu	Glu	Ala	Glu	Pro	Glu	Gly	Met	Phe	Lys	Ala	20	25	30	
Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val	35	40	45	
Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly	50	55	60	
Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val	65	70	75	
Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe	80	85	90	
Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu	95	100	105	
Thr	Ala	Lys	Ala	Gln	Lys	Met	Leu	Lys	Glu	Leu	Ile	Thr	Ser	Thr	110	115	120	
Arg	Leu	Gly	Thr	Tyr	Tyr	Asn	Ser	Ser	Ser	Val	Tyr	Ser	Phe	Gly	125	130	135	
Glu	Gly	Pro	Leu	Thr	Cys	Phe	Phe	Trp	Phe	Ile	Leu	Gln	Ile	Pro	140	145	150	
Glu	His	Arg	Arg	Leu	Met	Leu	Ser	Pro	Glu	Val	Val	Gln	Ala	Leu	155	160	165	
Leu	Val	Glu	Glu	Leu	Leu	Ser	Thr	Val	Asn	Ser	Ser	Ala	Ala	Val	170	175	180	
Pro	Tyr	Arg	Ala	Glu	Tyr	Glu	Val	Asp	Pro	Glu	Gly	Leu	Val	Ile	185	190	195	
Leu	Glu	Ala	Ser	Val	Lys	Asp	Ile	Ala	Ala	Leu	Asn	Ser	Thr	Leu	200	205	210	
Gly	Cys	Tyr	Arg	Tyr	Ser	Tyr	Val	Gly	Gln	Gly	Gln	Val	Leu	Arg	215	220	225	
Leu	Lys	Gly	Pro	Asp	His	Leu	Ala	Ser	Ser	Cys	Leu	Trp	His	Leu	230	235	240	
Gln	Gly	Pro	Lys	Asp	Leu	Met	Leu	Lys	Leu	Arg	Leu	Glu	Trp	Thr	245	250	255	
Leu	Ala	Glu	Cys	Arg	Asp	Arg	Leu	Ala	Met	Tyr	Asp	Val	Ala	Gly	260	265	270	
Pro	Leu	Glu	Lys	Arg	Leu	Ile	Thr	Ser	Val	Tyr	Gly	Cys	Ser	Arg	275	280	285	
Gln	Glu	Pro	Val	Val	Glu	Val	Leu	Ala	Ser	Gly	Ala	Ile	Met	Ala				

	290		295		300
Val Val Trp Lys	Lys Gly Leu His Ser	Tyr Tyr Asp Pro Phe	Val		
	305		310		315
Leu Ser Val Gln	Pro Val Val Phe Gln	Ala Cys Glu Val Asn	Leu		
	320		325		330
Thr Leu Asp Asn	Arg Leu Asp Ser Gln	Gly Val Leu Ser Thr	Pro		
	335		340		345
Tyr Phe Pro Ser	Tyr Tyr Ser Pro Gln	Thr His Cys Ser Trp	His		
	350		355		360
Leu Thr Val Pro	Ser Leu Asp Tyr Gly	Leu Ala Leu Trp Phe	Asp		
	365		370		375
Ala Tyr Ala Leu	Arg Arg Gln Lys Tyr	Asp Leu Pro Cys Thr	Gln		
	380		385		390
Gly Gln Trp Thr	Ile Gln Asn Arg Arg	Leu Cys Gly Leu Arg	Ile		
	395		400		405
Leu Gln Pro Tyr	Ala Glu Arg Ile Pro	Val Val Ala Thr Ala	Gly		
	410		415		420
Ile Thr Ile Asn	Phe Thr Ser Gln Ile	Ser Leu Thr Gly Pro	Gly		
	425		430		435
Val Arg Val His	Tyr Gly Leu Tyr Asn	Gln Ser Asp Pro Cys	Pro		
	440		445		450
Gly Glu Phe Leu	Cys Ser Val Asn Gly	Leu Cys Val Pro Ala	Cys		
	455		460		465
Asp Gly Val Lys	Asp Cys Pro Asn Gly	Leu Asp Glu Arg Asn	Cys		
	470		475		480
Val Cys Arg Ala	Thr Phe Gln Cys Lys	Glu Asp Ser Thr Cys	Ile		
	485		490		495
Ser Leu Pro Lys	Val Cys Asp Gly Gln	Pro Asp Cys Leu Asn	Gly		
	500		505		510
Ser Asp Glu Glu	Gln Cys Gln Glu Gly	Val Pro Cys Gly Thr	Phe		
	515		520		525
Thr Phe Gln Cys	Glu Asp Arg Ser Cys	Val Lys Lys Pro Asn	Pro		
	530		535		540
Gln Cys Asp Gly	Arg Pro Asp Cys Arg	Asp Gly Ser Asp Glu	Glu		
	545		550		555
His Cys Asp Cys	Gly Leu Gln Gly Pro	Ser Ser Arg Ile Val	Gly		
	560		565		570
Gly Ala Val Ser	Ser Glu Gly Glu Trp	Pro Trp Gln Ala Ser	Leu		
	575		580		585

Gln	Val	Arg	Gly	Arg	His	Ile	Cys	Gly	Gly	Ala	Leu	Ile	Ala	Asp	
				590					595					600	
Arg	Trp	Val	Ile	Thr	Ala	Ala	His	Cys	Phe	Gln	Glu	Asp	Ser	Met	
				605					610					615	
Ala	Ser	Thr	Val	Leu	Trp	Thr	Val	Phe	Leu	Gly	Lys	Val	Trp	Gln	
				620					625					630	
Asn	Ser	Arg	Trp	Pro	Gly	Glu	Val	Ser	Phe	Lys	Val	Ser	Arg	Leu	
				635					640					645	
Leu	Leu	His	Pro	Tyr	His	Glu	Glu	Asp	Ser	His	Asp	Tyr	Asp	Val	
				650					655					660	
Ala	Leu	Leu	Gln	Leu	Asp	His	Pro	Val	Val	Arg	Ser	Ala	Ala	Val	
				665					670					675	
Arg	Pro	Val	Cys	Leu	Pro	Ala	Arg	Ser	His	Phe	Phe	Glu	Pro	Gly	
				680					685					690	
Leu	His	Cys	Trp	Ile	Thr	Gly	Trp	Gly	Ala	Leu	Arg	Glu	Gly	Gly	
				695					700					705	
Pro	Ile	Ser	Asn	Ala	Leu	Gln	Lys	Val	Asp	Val	Gln	Leu	Ile	Pro	
				710					715					720	
Gln	Asp	Leu	Cys	Ser	Glu	Ala	Tyr	Arg	Tyr	Gln	Val	Thr	Pro	Arg	
				725					730					735	
Met	Leu	Cys	Ala	Gly	Tyr	Arg	Lys	Gly	Lys	Lys	Asp	Ala	Cys	Gln	
				740					745					750	
Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Lys	Ala	Leu	Ser	Gly	Arg	
				755					760					765	
Trp	Phe	Leu	Ala	Gly	Leu	Val	Ser	Trp	Gly	Leu	Gly	Cys	Gly	Arg	
				770					775					780	
Pro	Asn	Tyr	Phe	Gly	Val	Tyr	Thr	Arg	Ile	Thr	Gly	Val	Ile	Ser	
				785					790					795	
Trp	Ile	Gln	Gln	Val	Val	Thr									
				800											

<210> 170
 <211> 1327
 <212> DNA
 <213> Homo sapiens

<400> 170
 gcacccaggg ccagtggacg atccagaaca ggaggctgtg tggcttgccg 50
 atcctgcagc cctacgccga gaggatcccc gtggtggcca cggccgggat 100
 caccatcaac ttcacctccc agatctccct caccgggccc ggtgtgcggg 150
 tgcactatgg cttgtacaac cagtcggacc cctgccctgg agagttcctc 200

tgttctgtga atggactctg tgtccctgcc tgtgatgggg tcaaggactg 250
 cccaacggc ctggatgaga gaaactgcgt ttgcagagcc acattccagt 300
 gcaaagagga cagcacatgc atctcactgc ccaaggtctg tgatgggcag 350
 cctgattgtc tcaacggcag cgatgaagag cagtgccagg aaggggtgcc 400
 atgtgggaca ttcaccttcc agtgtgagga ccggagctgc gtgaagaagc 450
 ccaacccgca gtgtgatggg cggcccgact gcagggacgg ctcggatgag 500
 gagcactgtg actgtggcct ccagggcccc tccagccgca ttgttgggtg 550
 agctgtgtcc tccgaggggt agtggccatg gcaggccagc ctccagggtc 600
 ggggtcgaca catctgtggg ggggccctca tcgctgaccg ctgggtgata 650
 acagctgccc actgcttcca ggaggacagc atggcctcca cgggtgctgtg 700
 gaccgtgttc ctgggcaagg tgtggcagaa ctgcgctgg cctggagagg 750
 tgtccttcaa ggtgagccgc ctgctcctgc acccgtagca cgaagaggac 800
 agccatgact acgacgtggc gctgctgcag ctcgaccacc cgggtgtgag 850
 ctcgcccgcc gtgcgccccg tctgcctgcc cgcgcgctcc cacttcttcg 900
 agcccggcct gcaactgctg attacgggct ggggcgcctt gcgcgagggc 950
 ggccccatca gcaacgctct gcagaaagtg gatgtgcagt tgatcccaca 1000
 ggacctgtgc agcgaggcct atcgctacca ggtgacgcca cgcagtctgt 1050
 gtgccggcta ccgcaagggc aagaaggatg cctgtcaggg tgactcaggt 1100
 ggtccgctgg tgtgcaaggc actcagtggc cgctggttcc tggcggggct 1150
 ggtcagctgg ggccctgggct gtggccggcc taactacttc ggcgctctaca 1200
 cccgcatcac aggtgtgatc agctggatcc agcaagtggg gacctgagga 1250
 actgcccccc tgcaaagcag ggcccacctc ctggactcag agagcccagg 1300
 gcaactgcca agcaggggga caagtat 1327

<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taacagctgc cactgcttc cagg 24

<210> 172

<211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 172
 taatccagca gtgcaggccg gg 22

 <210> 173
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 173
 atggcctcca cgggtgctgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

 <210> 174
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 174
 tgcctatgca ctgaggaggc agaag 25

 <210> 175
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 175
 aggcagggac acagagtcca ttcac 25

 <210> 176
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 176
 agtatgattt gccgtgcacc cagggccagt ggacgatcca gaacaggagg 50

 <210> 177
 <211> 1510
 <212> DNA
 <213> Homo sapiens

<400> 177

ggacgagggc agatctcgtt ctggggcaag ccgttgacac tcgctccctg 50
ccaccgcccg ggctccgtgc cgccaagttt tcattttcca ctttctctgc 100
ctccagtccc ccagcccctg gccgagagaa gggctcttacc ggccgggatt 150
gctggaaaca ccaagaggtg gtttttgttt tttaaaactt ctgtttcttg 200
ggaggggggtg tggcggggca ggatgagcaa ctccgttcct ctgctctgtt 250
tctggagcct ctgctattgc tttgctgcgg ggagccccgt accttttggg 300
ccagagggac ggctggaaga taagctccac aaacccaaag ctacacagac 350
tgaggtcaaa ccatctgtga ggtttaacct ccgcacctcc aaggaccag 400
agcatgaagg atgctacctc tccgtcggcc acagccagcc cttagaagac 450
tgcagtttca acatgacagc taaaaccttt ttcattcattc acggatggac 500
gatgagcggg atctttgaaa actggctgca caaactcgtg tcagccctgc 550
acacaagaga gaaagacgcc aatgtagttg tggttgactg gctccccctg 600
gccaccagc tttacacgga tgcgggtcaat aataccaggg tgggtgggaca 650
cagcattgcc aggatgctcg actggctgca ggagaaggac gatttttctc 700
tcgggaatgt ccacttgatc ggctacagcc tcggagcgca cgtggccggg 750
tatgcaggca acttcgtgaa aggaacggtg ggccgaatca caggtttga 800
tcctgccggg cccatgtttg aaggggccga catccacaag aggtctctc 850
cggacgatgc agattttgtg gatgtcctcc acacctacac gcgttccttc 900
ggcttgagca ttggtattca gatgcctgtg ggccacattg acatctaccc 950
caatgggggt gacttcagc caggctgtgg actcaacgat gtcttgggat 1000
caattgcata tggaacaatc acagaggtgg taaaatgtga gcatgagcga 1050
gccgtccacc tctttgttga ctctctggg aatcaggaca agccgagttt 1100
tgcottccag tgcactgact ccaatcgctt caaaaagggg atctgtctga 1150
gctgccgcaa gaaccgttgt aatagcattg gctacaatgc caagaaaatg 1200
aggaacaaga ggaacagcaa aatgtaccta aaaacccggg caggcatgcc 1250
tttcagaggt aaccttcagt ccctggagt tccctgagga aggcccttaa 1300
tacctccttc ttaataccat gctgcagagc agggcacatc ctagcccagg 1350
agaagtggcc agcacaatcc aatcaaactg ttgcaaata gattacactg 1400
tgcatgtcct aggaagggga atctttacaa aataaacagt gtggaccct 1450

aataaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500

aaaaaaaaaa 1510

<210> 178

<211> 354

<212> PRT

<213> Homo sapiens

<400> 178

Met	Ser	Asn	Ser	Val	Pro	Leu	Leu	Cys	Phe	Trp	Ser	Leu	Cys	Tyr
1				5					10					15

Cys	Phe	Ala	Ala	Gly	Ser	Pro	Val	Pro	Phe	Gly	Pro	Glu	Gly	Arg
				20					25					30

Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val
				35					40					45

Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu
				50					55					60

His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu
				65					70					75

Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His
				80					85					90

Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu
				95					100					105

Val	Ser	Ala	Leu	His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val
				110					115					120

Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val
				125					130					135

Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp
				140					145					150

Trp	Leu	Gln	Glu	Lys	Asp	Asp	Phe	Ser	Leu	Gly	Asn	Val	His	Leu
				155					160					165

Ile	Gly	Tyr	Ser	Leu	Gly	Ala	His	Val	Ala	Gly	Tyr	Ala	Gly	Asn
				170					175					180

Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	Thr	Gly	Leu	Asp	Pro	Ala
				185					190					195

Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	Lys	Arg	Leu	Ser	Pro
				200					205					210

Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	Tyr	Thr	Arg	Ser
				215					220					225

Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	His	Ile	Asp
				230					235					240

Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn
				245					250					255
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val
				260					265					270
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu
				275					280					285
Val	Asn	Gln	Asp	Lys	Pro	Ser	Phe	Ala	Phe	Gln	Cys	Thr	Asp	Ser
				290					295					300
Asn	Arg	Phe	Lys	Lys	Gly	Ile	Cys	Leu	Ser	Cys	Arg	Lys	Asn	Arg
				305					310					315
Cys	Asn	Ser	Ile	Gly	Tyr	Asn	Ala	Lys	Lys	Met	Arg	Asn	Lys	Arg
				320					325					330
Asn	Ser	Lys	Met	Tyr	Leu	Lys	Thr	Arg	Ala	Gly	Met	Pro	Phe	Arg
				335					340					345
Gly	Asn	Leu	Gln	Ser	Leu	Glu	Cys	Pro						
				350										

<210> 179

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

gtgagcatga gcgagccgtc cac 23

<210> 180

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 180

gctattacaa cggttcttgc ggcagc 26

<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

ttgactctct ggtgaatcag gacaagccga gttttgcctt ccag 44

<210> 182

<211> 3240
<212> DNA
<213> Homo sapiens

<400> 182

cgagacgcgtg ggcggaacgc tgggcctggg caagggccgg ggcgccgggc 50
cgagccacct ctccccctcc cccgcttccc tgtcgcgctc cgtgggctgg 100
acgcgctgga ggagtggagc agcaccgggc cggccctggg ggctgacagt 150
cggcaaagtt tggcccgaag aggaagtggc ctcaaaccgc ggcaggtggc 200
gaccaggcca gaccaggggc gctcgtgccc tgcgggcggg ctgtaggcga 250
gggcgcgccc cagtgcgag acccggggct tcaggagccg gccccgggag 300
agaagagtgc ggcggcggac ggagaaaaca actccaaagt tggcgaaagg 350
caccgcccct actccgggac tgcgcgcgcc tccccgcccc cagccctggc 400
atccagagta cgggtcgagc ccgggccatg gagccccct ggggaggcgg 450
caccagggag cctggggccc cggggctccg ccgcgacccc atcgggtaga 500
ccacagaagc tccgggaccc ttccggcacc tctggacagc ccaggatgct 550
gttggccacc ctctctctcc tctccttgg aggcgctctg gcccatccag 600
accggattat ttttccaaat catgcttgtg aggaccccc agcagtgtc 650
ttagaagtgc agggcacctt acagaggccc ctggtccggg acagccgcac 700
ctccccctgc aactgcacct ggctcatcct gggcagcaag gaacagactg 750
tcaccatcag gttccagaag ctacacctgg cctgtggctc agagcgctta 800
accctacgct cccctctcca gccactgatc tcctgtgtg aggcacctcc 850
cagccctctg cagctgcccg ggggcaacgt caccatcact tacagctatg 900
ctggggccag agcaccatg ggccagggct tcctgctctc ctacagccaa 950
gattggctga tgtgcctgca ggaagagttt cagtgcctga accaccgctg 1000
tgtatctgct gtccagcgt gtgatggggg tgatgcctgt ggcgatggct 1050
ctgatgaagc aggttgagc tcagaccct tccctggcct gaccccaaga 1100
ccgctccct cctgccttg caatgtcacc ttggaggact tctatgggg 1150
cttctctct cctggatata cacacctagc ctcatgtctc cccccagt 1200
cctgccattg gctgctggac cccatgatg gccggcggct ggccgtgcgc 1250
ttcacagccc tggacttggg ctttggagat gcagtgcagc tgtatgacgg 1300
ccctgggccc cctgagagct cccgactact gcgtagtctc acccacttca 1350

ttcaggggact tgggtgggcct cccgttgacc ctatgtagct gctataaaagt 2850
 taagtgtccc tcaggcaggg agaggggtca cagagtctcc tctgtacgtg 2900
 gccatggcca gacaccccag tcccttcacc accacctgct ccccacgcca 2950
 ccaccatttg ggtggctggt tttaaaaagt aaagttctta gaggatcata 3000
 ggtctggaca ctccatcctt gccaaacctc tacccaaaag tggccttaag 3050
 caccggaatg ccaattaact agagaccctc cagcccccaa ggggaggatt 3100
 tgggcagaac ctgaggtttt gccatccaca atccctccta cagggcctgg 3150
 ctcacaaaaa gagtgaaca aatgcttcta ttccatagct acggcattgc 3200
 tcagtaagtt gagggtcaaaa ataaaggaat catacatctc 3240

<210> 183

<211> 713

<212> PRT

<213> Homo sapiens

<400> 183

Met Leu Leu Ala Thr Leu Leu Leu Leu Leu Leu Gly Gly Ala Leu
 1 5 10 15

Ala His Pro Asp Arg Ile Ile Phe Pro Asn His Ala Cys Glu Asp
 20 25 30

Pro Pro Ala Val Leu Leu Glu Val Gln Gly Thr Leu Gln Arg Pro
 35 40 45

Leu Val Arg Asp Ser Arg Thr Ser Pro Ala Asn Cys Thr Trp Leu
 50 55 60

Ile Leu Gly Ser Lys Glu Gln Thr Val Thr Ile Arg Phe Gln Lys
 65 70 75

Leu His Leu Ala Cys Gly Ser Glu Arg Leu Thr Leu Arg Ser Pro
 80 85 90

Leu Gln Pro Leu Ile Ser Leu Cys Glu Ala Pro Pro Ser Pro Leu
 95 100 105

Gln Leu Pro Gly Gly Asn Val Thr Ile Thr Tyr Ser Tyr Ala Gly
 110 115 120

Ala Arg Ala Pro Met Gly Gln Gly Phe Leu Leu Ser Tyr Ser Gln
 125 130 135

Asp Trp Leu Met Cys Leu Gln Glu Glu Phe Gln Cys Leu Asn His
 140 145 150

Arg Cys Val Ser Ala Val Gln Arg Cys Asp Gly Val Asp Ala Cys
 155 160 165

Gly Asp Gly Ser Asp Glu Ala Gly Cys Ser Ser Asp Pro Phe Pro

	170		175		180
Gly Leu Thr Pro Arg Pro Val Pro Ser	185	Leu Pro Cys Asn Val Thr	190		195
Leu Glu Asp Phe Tyr Gly Val Phe Ser	200	Ser Pro Gly Tyr Thr His	205		210
Leu Ala Ser Val Ser His Pro Gln Ser	215	Cys His Trp Leu Leu Asp	220		225
Pro His Asp Gly Arg Arg Leu Ala Val	230	Arg Phe Thr Ala Leu Asp	235		240
Leu Gly Phe Gly Asp Ala Val His Val	245	Tyr Asp Gly Pro Gly Pro	250		255
Pro Glu Ser Ser Arg Leu Leu Arg Ser	260	Leu Thr His Phe Ser Asn	265		270
Gly Lys Ala Val Thr Val Glu Thr Leu	275	Ser Gly Gln Ala Val Val	280		285
Ser Tyr His Thr Val Ala Trp Ser Asn	290	Gly Arg Gly Phe Asn Ala	295		300
Thr Tyr His Val Arg Gly Tyr Cys Leu	305	Pro Trp Asp Arg Pro Cys	310		315
Gly Leu Gly Ser Gly Leu Gly Ala Gly	320	Glu Gly Leu Gly Glu Arg	325		330
Cys Tyr Ser Glu Ala Gln Arg Cys Asp	335	Gly Ser Trp Asp Cys Ala	340		345
Asp Gly Thr Asp Glu Glu Asp Cys Pro	350	Gly Cys Pro Pro Gly His	355		360
Phe Pro Cys Gly Ala Ala Gly Thr Ser	365	Gly Ala Thr Ala Cys Tyr	370		375
Leu Pro Ala Asp Arg Cys Asn Tyr Gln	380	Thr Phe Cys Ala Asp Gly	385		390
Ala Asp Glu Arg Arg Cys Arg His Cys	395	Gln Pro Gly Asn Phe Arg	400		405
Cys Arg Asp Glu Lys Cys Val Tyr Glu	410	Thr Trp Val Cys Asp Gly	415		420
Gln Pro Asp Cys Ala Asp Gly Ser Asp	425	Glu Trp Asp Cys Ser Tyr	430		435
Val Leu Pro Arg Lys Val Ile Thr Ala	440	Ala Val Ile Gly Ser Leu	445		450
Val Cys Gly Leu Leu Leu Val Ile Ala	455	Leu Gly Cys Thr Cys Lys	460		465

Leu	Tyr	Ala	Ile	Arg	Thr	Gln	Glu	Tyr	Ser	Ile	Phe	Ala	Pro	Leu	
				470					475					480	
Ser	Arg	Met	Glu	Ala	Glu	Ile	Val	Gln	Gln	Gln	Ala	Pro	Pro	Ser	
				485					490					495	
Tyr	Gly	Gln	Leu	Ile	Ala	Gln	Gly	Ala	Ile	Pro	Pro	Val	Glu	Asp	
				500					505					510	
Phe	Pro	Thr	Glu	Asn	Pro	Asn	Asp	Asn	Ser	Val	Leu	Gly	Asn	Leu	
				515					520					525	
Arg	Ser	Leu	Leu	Gln	Ile	Leu	Arg	Gln	Asp	Met	Thr	Pro	Gly	Gly	
				530					535					540	
Gly	Pro	Gly	Ala	Arg	Arg	Arg	Gln	Arg	Gly	Arg	Leu	Met	Arg	Arg	
				545					550					555	
Leu	Val	Arg	Arg	Leu	Arg	Arg	Trp	Gly	Leu	Leu	Pro	Arg	Thr	Asn	
				560					565					570	
Thr	Pro	Ala	Arg	Ala	Ser	Glu	Ala	Arg	Ser	Gln	Val	Thr	Pro	Ser	
				575					580					585	
Ala	Ala	Pro	Leu	Glu	Ala	Leu	Asp	Gly	Gly	Thr	Gly	Pro	Ala	Arg	
				590					595					600	
Glu	Gly	Gly	Ala	Val	Gly	Gly	Gln	Asp	Gly	Glu	Gln	Ala	Pro	Pro	
				605					610					615	
Leu	Pro	Ile	Lys	Ala	Pro	Leu	Pro	Ser	Ala	Ser	Thr	Ser	Pro	Ala	
				620					625					630	
Pro	Thr	Thr	Val	Pro	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Ser	Leu	Pro	
				635					640					645	
Leu	Glu	Pro	Ser	Leu	Leu	Ser	Gly	Val	Val	Gln	Ala	Leu	Arg	Gly	
				650					655					660	
Arg	Leu	Leu	Pro	Ser	Leu	Gly	Pro	Pro	Gly	Pro	Thr	Arg	Ser	Pro	
				665					670					675	
Pro	Gly	Pro	His	Thr	Ala	Val	Leu	Ala	Leu	Glu	Asp	Glu	Asp	Asp	
				680					685					690	
Val	Leu	Leu	Val	Pro	Leu	Ala	Glu	Pro	Gly	Val	Trp	Val	Ala	Glu	
				695					700					705	
Ala	Glu	Asp	Glu	Pro	Leu	Leu	Thr								
				710											

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184
ggctgtcact gtggagacac 20

<210> 185
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
gcaaggtcat tacagctg 18

<210> 186
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
agaacatagg agcagtccca ctc 23

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 187
tgcctgctgc tgcacaatct cag 23

<210> 188
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 188
ggctattgct tgccttgga cagaccctgt ggcttaggct ctggc 45

<210> 189
<211> 663
<212> DNA
<213> Homo sapiens

<400> 189
cgagctgggc gagaagtagg ggagggcggt gctccgccgc ggtggcggtt 50
gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100
gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150

aataaaacat cgcccccttct gcttcagtgt gaaaggccac gtgaagatgc 200
tgcggctggc actaactgtg acatctatga ccttttttat catcgacaaa 250
gcccctgaac catatatgtg tatcactgga tttgaagtca ccgttatctt 300
atttttcata ctttttatatg tactcagact tgatcgatta atgaagtggg 350
tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400
atgctcatcg tatctgtgtt ggcactgata ccagaaacca caacattgac 450
agttgggtgga ggggtgtttg cacttgtgac agcagtatgc tgtcttgccg 500
acgggggccct tatttaccgg aagcttctgt tcaatcccag cggtccttac 550
cagaaaaagc ctgtgcatga aaaaaaagaa gttttgtaat tttatattac 600
tttttagttt gatactaagt attaaacata tttctgtatt cttccaaaaa 650
aaaaaaaaaa aaa 663

<210> 190
<211> 152
<212> PRT
<213> Homo sapiens
<400> 190
Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe
1 5 10 15
Ser Val Lys Gly His Val Lys Met Leu Arg Leu Ala Leu Thr Val
20 25 30
Thr Ser Met Thr Phe Phe Ile Ile Ala Gln Ala Pro Glu Pro Tyr
35 40 45
Ile Val Ile Thr Gly Phe Glu Val Thr Val Ile Leu Phe Phe Ile
50 55 60
Leu Leu Tyr Val Leu Arg Leu Asp Arg Leu Met Lys Trp Leu Phe
65 70 75
Trp Pro Leu Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe
80 85 90
Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr
95 100 105
Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys
110 115 120
Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn
125 130 135
Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
140 145 150

Val Leu

<210> 191
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 212, 234, 487
<223> unknown base

<400> 191
gggcgagaag taggggaggg cgtgttccgc cgcggtggcg gttgctatcg 50
ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100
ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150
catcgcccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200
ggcactaact gngacatcta tgaccttttt tatnatcgca caagcccctg 250
aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300
atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350
gcctttgctt gatattatca actcactggt aacaacagta ttcattgtca 400
tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggt 450
ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 192
cgttttgcag aacctactca ggcag 25

<210> 193
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 193
cctccaccaa ctgtcaatgt tgtgg 25

<210> 194
<211> 40

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 194
aaagtgctgc tgctgggtct gcagacgcga tggataacgt 40

<210> 195
<211> 1879
<212> DNA
<213> Homo sapien

<400> 195
cagccccgcg cgccggccga gtcgtgagc cgcggctgcc ggacgggacg 50
ggaccggcta ggctggggcg gccccccggg ccccgccgtg ggcatgggag 100
caactggcccc ggctgtgtgt ctgcctctgc tggcccagtg gtccttgcgc 150
gccgcccccg agctggcccc cgcgcccttc acgtgcccc tccgggtggc 200
cgcgggccacg aaccgcgtag ttgcgccac cccgggaccc gggacccctg 250
ccgagcgcca cgccgacggc ttggcgctcg ccctggagcc tgccttggcg 300
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 caccgctctt caatctctgt tctgctccca gatgccttct agattcactg 1800
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 aaataattaa aaaaaaact tcattctaa 1879

<210> 196
 <211> 518
 <212> PRT
 <213> Homo sapien

<400> 196
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 Trp Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr
 20 25 30
 Leu Pro Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro
 35 40 45
 Thr Pro Gly Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu
 50 55 60
 Ala Leu Ala Leu Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala
 65 70 75
 Asn Phe Leu Ala Met Val Asp Asn Leu Gln Gly Asp Ser Gly Arg
 80 85 90
 Gly Tyr Tyr Leu Glu Met Leu Ile Gly Thr Pro Pro Gln Lys Leu
 95 100 105

Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly	110	115	120
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser	125	130	135
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr	140	145	150
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile	155	160	165
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile	170	175	180
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly	185	190	195
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser	200	205	210
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro	215	220	225
Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala	230	235	240
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu	245	250	255
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu	260	265	270
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly	275	280	285
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Glu	Tyr	Asn	Ala	Asp	Lys	Ala	290	295	300
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val	305	310	315
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro	320	325	330
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp	335	340	345
Thr	Asn	Ser	Glu	Thr	Pro	Trp	Ser	Tyr	Phe	Pro	Lys	Ile	Ser	Ile	350	355	360
Tyr	Leu	Arg	Asp	Glu	Asn	Ser	Ser	Arg	Ser	Phe	Arg	Ile	Thr	Ile	365	370	375
Leu	Pro	Gln	Leu	Tyr	Ile	Gln	Pro	Met	Met	Gly	Ala	Gly	Leu	Asn	380	385	390
Tyr	Glu	Cys	Tyr	Arg	Phe	Gly	Ile	Ser	Pro	Ser	Thr	Asn	Ala	Leu			

	395	400	405
Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr Val Ile Phe Asp	410	415	420
Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro Cys Ala Glu	425	430	435
Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe Ser Thr	440	445	450
Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser Glu	455	460	465
Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly	470	475	480
Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg	485	490	495
Cys Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser	500	505	510
Ser Leu Val Arg His Arg Trp Lys	515		

<210> 197

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 197

cgcagaagct acagattctc g 21

<210> 198

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 198

ggaaattgga ggccaaagc 19

<210> 199

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 199

ggatgtagcc agcaactgtg 20

<210> 200
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 200
gccttggctc gttctcttc 19

<210> 201
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 201
ggtcctgtgc ctggatgg 18

<210> 202
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 202
gacaagacta cctccgttgg tc 22

<210> 203
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 203
tgatgcacag ttcagcacct gttg 24

<210> 204
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 204
cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205
<211> 1939
<212> DNA

<213> Homo sapiens

<400> 205

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gggcgggagc cgggaggcgc ggccggcatg gaggcgctgc tgctgggcgc 150
ggggttgctg ctgggcgctt acgtgcttgt ctactacaac ctggtgaagg 200
ccccgcgctg cggcggcatg ggcaacctgc ggggccgcac ggccgtggtc 250
acgggcgcca acagcggcat cggaaagatg acggcgctgg agctggcgcg 300
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 cagggcaggg cagctggtat cgaggtgccc catgggagta aggggacgcc 1850
 ttccgggagg atgcagggtt ggggtcatct gtatctgaag cccctcggaa 1900
 taaagcgcgt tgaccgcca aaaaaaaaaa aaaaaaaaaa 1939

<210> 206
 <211> 377
 <212> PRT
 <213> Homo sapiens

<400> 206
 Met Glu Ala Leu Leu Leu Gly Ala Gly Leu Leu Leu Gly Ala Tyr
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 Val Leu Val Tyr Tyr Asn Leu Val Lys Ala Pro Pro Cys Gly Gly
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 Met Gly Asn Leu Arg Gly Arg Thr Ala Val Val Thr Gly Ala Asn
 35 40 45
 Ser Gly Ile Gly Lys Met Thr Ala Leu Glu Leu Ala Arg Arg Gly
 50 55 60
 Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg Gly Glu Ala
 65 70 75
 Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile
 80 85 90
 Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe
 95 100 105
 Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile
 110 115 120
 His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe
 125 130 135
 Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr
 140 145 150

His	Leu	Leu	Leu	Pro	Cys	Leu	Lys	Ala	Cys	Ala	Pro	Ser	Arg	Val	
				155					160					165	
Val	Val	Val	Ala	Ser	Ala	Ala	His	Cys	Arg	Gly	Arg	Leu	Asp	Phe	
				170					175					180	
Lys	Arg	Leu	Asp	Arg	Pro	Val	Val	Gly	Trp	Arg	Gln	Glu	Leu	Arg	
				185					190					195	
Ala	Tyr	Ala	Asp	Thr	Lys	Leu	Ala	Asn	Val	Leu	Phe	Ala	Arg	Glu	
				200					205					210	
Leu	Ala	Asn	Gln	Leu	Glu	Ala	Thr	Gly	Val	Thr	Cys	Tyr	Ala	Ala	
				215					220					225	
His	Pro	Gly	Pro	Val	Asn	Ser	Glu	Leu	Phe	Leu	Arg	His	Val	Pro	
				230					235					240	
Gly	Trp	Leu	Arg	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Trp	Leu	Val	Leu	
				245					250					255	
Arg	Ala	Pro	Arg	Gly	Gly	Ala	Gln	Thr	Pro	Leu	Tyr	Cys	Ala	Leu	
				260					265					270	
Gln	Glu	Gly	Ile	Glu	Pro	Leu	Ser	Gly	Arg	Tyr	Phe	Ala	Asn	Cys	
				275					280					285	
His	Val	Glu	Glu	Val	Pro	Pro	Ala	Ala	Arg	Asp	Asp	Arg	Ala	Ala	
				290					295					300	
His	Arg	Leu	Trp	Glu	Ala	Ser	Lys	Arg	Leu	Ala	Gly	Leu	Gly	Pro	
				305					310					315	
Gly	Glu	Asp	Ala	Glu	Pro	Asp	Glu	Asp	Pro	Gln	Ser	Glu	Asp	Ser	
				320					325					330	
Glu	Ala	Pro	Ser	Ser	Leu	Ser	Thr	Pro	His	Pro	Glu	Glu	Pro	Thr	
				335					340					345	
Val	Ser	Gln	Pro	Tyr	Pro	Ser	Pro	Gln	Ser	Ser	Pro	Asp	Leu	Ser	
				350					355					360	
Lys	Met	Thr	His	Arg	Ile	Gln	Ala	Lys	Val	Glu	Pro	Glu	Ile	Gln	
				365					370					375	

Leu Ser

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

cttcatggcc ttggacttgg ccag 24

[illegible]

<213> Artificial Sequence

acgccagtgg cctcaagctg gttg 24

<213> Artificial Sequence

ctttctgagc tctgagccac gggtggacat cctcatccac aatgc 45

<213> Homo sapiens

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cctgcagagg gccccaagcc tagaccggcg gtgtggctca gctggaaggt 800
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cttaagaaat ttgataccat aaaatggtaa aaaaaaaaaa aaaaaaaaaa 3700

aaaaaaaaaa aaaaaa 3716

<210> 211

<211> 985

<212> PRT

<213> Homo sapiens

<400> 211

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Pro	Gln	Asp	Gln	Leu	Phe	Gln	Gly	Pro	Gly	Pro	Ala	Arg	Met	Ser
			20				25							30

Cys	Gln	Ala	Ser	Gly	Gln	Pro	Pro	Pro	Thr	Ile	Arg	Trp	Leu	Leu
				35					40					45

Asn	Gly	Gln	Pro	Leu	Ser	Met	Val	Pro	Pro	Asp	Pro	His	His	Leu
				50					55					60

Leu	Pro	Asp	Gly	Thr	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Ala	Arg	Gly
				65					70					75

His	Ala	His	Asp	Gly	Gln	Ala	Leu	Ser	Thr	Asp	Leu	Gly	Val	Tyr
				80					85					90

Thr	Cys	Glu	Ala	Ser	Asn	Arg	Leu	Gly	Thr	Ala	Val	Ser	Arg	Gly
				95					100					105

Ala	Arg	Leu	Ser	Val	Ala	Val	Leu	Arg	Glu	Asp	Phe	Gln	Ile	Gln
				110					115					120

Pro	Arg	Asp	Met	Val	Ala	Val	Val	Gly	Glu	Gln	Phe	Thr	Leu	Glu
				125					130					135

Cys	Gly	Pro	Pro	Trp	Gly	His	Pro	Glu	Pro	Thr	Val	Ser	Trp	Trp
				140					145					150

Lys	Asp	Gly	Lys	Pro	Leu	Ala	Leu	Gln	Pro	Gly	Arg	His	Thr	Val
				155					160					165

Ser	Gly	Gly	Ser	Leu	Leu	Met	Ala	Arg	Ala	Glu	Lys	Ser	Asp	Glu
				170					175					180

Gly	Thr	Tyr	Met	Cys	Val	Ala	Thr	Asn	Ser	Ala	Gly	His	Arg	Glu
				185					190					195

Ser	Arg	Ala	Ala	Arg	Val	Ser	Ile	Gln	Glu	Pro	Gln	Asp	Tyr	Thr
				200					205					210

Glu	Pro	Val	Glu	Leu	Leu	Ala	Val	Arg	Ile	Gln	Leu	Glu	Asn	Val
				215					220					225

Thr	Leu	Leu	Asn	Pro	Asp	Pro	Ala	Glu	Gly	Pro	Lys	Pro	Arg	Pro
				230					235					240

Ala	Val	Trp	Leu	Ser	Trp	Lys	Val	Ser	Gly	Pro	Ala	Ala	Pro	Ala	
				245					250					255	
Gln	Ser	Tyr	Thr	Ala	Leu	Phe	Arg	Thr	Gln	Thr	Ala	Pro	Gly	Gly	
				260					265					270	
Gln	Gly	Ala	Pro	Trp	Ala	Glu	Glu	Leu	Leu	Ala	Gly	Trp	Gln	Ser	
				275					280					285	
Ala	Glu	Leu	Gly	Gly	Leu	His	Trp	Gly	Gln	Asp	Tyr	Glu	Phe	Lys	
				290					295					300	
Val	Arg	Pro	Ser	Ser	Gly	Arg	Ala	Arg	Gly	Pro	Asp	Ser	Asn	Val	
				305					310					315	
Leu	Leu	Leu	Arg	Leu	Pro	Glu	Lys	Val	Pro	Ser	Ala	Pro	Pro	Gln	
				320					325					330	
Glu	Val	Thr	Leu	Lys	Pro	Gly	Asn	Gly	Thr	Val	Phe	Val	Ser	Trp	
				335					340					345	
Val	Pro	Pro	Pro	Ala	Glu	Asn	His	Asn	Gly	Ile	Ile	Arg	Gly	Tyr	
				350					355					360	
Gln	Val	Trp	Ser	Leu	Gly	Asn	Thr	Ser	Leu	Pro	Pro	Ala	Asn	Trp	
				365					370					375	
Thr	Val	Val	Gly	Glu	Gln	Thr	Gln	Leu	Glu	Ile	Ala	Thr	His	Met	
				380					385					390	
Pro	Gly	Ser	Tyr	Cys	Val	Gln	Val	Ala	Ala	Val	Thr	Gly	Ala	Gly	
				395					400					405	
Ala	Gly	Glu	Pro	Ser	Arg	Pro	Val	Cys	Leu	Leu	Leu	Glu	Gln	Ala	
				410					415					420	
Met	Glu	Arg	Ala	Thr	Gln	Glu	Pro	Ser	Glu	His	Gly	Pro	Trp	Thr	
				425					430					435	
Leu	Glu	Gln	Leu	Arg	Ala	Thr	Leu	Lys	Arg	Pro	Glu	Val	Ile	Ala	
				440					445					450	
Thr	Cys	Gly	Val	Ala	Leu	Trp	Leu	Leu	Leu	Leu	Gly	Thr	Ala	Val	
				455					460					465	
Cys	Ile	His	Arg	Arg	Arg	Arg	Ala	Arg	Val	His	Leu	Gly	Pro	Gly	
				470					475					480	
Leu	Tyr	Arg	Tyr	Thr	Ser	Glu	Asp	Ala	Ile	Leu	Lys	His	Arg	Met	
				485					490					495	
Asp	His	Ser	Asp	Ser	Gln	Trp	Leu	Ala	Asp	Thr	Trp	Arg	Ser	Thr	
				500					505					510	
Ser	Gly	Ser	Arg	Asp	Leu	Ser	Ser	Ser	Ser	Ser	Leu	Ser	Ser	Arg	
				515					520					525	
Leu	Gly	Ala	Asp	Ala	Arg	Asp	Pro	Leu	Asp	Cys	Arg	Arg	Ser	Leu	

	530		535		540
Leu Ser Trp Asp	Ser Arg Ser Pro Gly	Val Pro Leu Leu Pro	Asp		
	545	550	555		
Thr Ser Thr Phe	Tyr Gly Ser Leu Ile	Ala Glu Leu Pro Ser	Ser		
	560	565	570		
Thr Pro Ala Arg	Pro Ser Pro Gln Val	Pro Ala Val Arg Arg	Leu		
	575	580	585		
Pro Pro Gln Leu	Ala Gln Leu Ser Ser	Pro Cys Ser Ser Ser	Asp		
	590	595	600		
Ser Leu Cys Ser	Arg Arg Gly Leu Ser	Ser Pro Arg Leu Ser	Leu		
	605	610	615		
Ala Pro Ala Glu	Ala Trp Lys Ala Lys	Lys Lys Gln Glu Leu	Gln		
	620	625	630		
His Ala Asn Ser	Ser Pro Leu Leu Arg	Gly Ser His Ser Leu	Glu		
	635	640	645		
Leu Arg Ala Cys	Glu Leu Gly Asn Arg	Gly Ser Lys Asn Leu	Ser		
	650	655	660		
Gln Ser Pro Gly	Ala Val Pro Gln Ala	Leu Val Ala Trp Arg	Ala		
	665	670	675		
Leu Gly Pro Lys	Leu Leu Ser Ser Ser	Asn Glu Leu Val Thr	Arg		
	680	685	690		
His Leu Pro Pro	Ala Pro Leu Phe Pro	His Glu Thr Pro Pro	Thr		
	695	700	705		
Gln Ser Gln Gln	Thr Gln Pro Pro Val	Ala Pro Gln Ala Pro	Ser		
	710	715	720		
Ser Ile Leu Leu	Pro Ala Ala Pro Ile	Pro Ile Leu Ser Pro	Cys		
	725	730	735		
Ser Pro Pro Ser	Pro Gln Ala Ser Ser	Leu Ser Gly Pro Ser	Pro		
	740	745	750		
Ala Ser Ser Arg	Leu Ser Ser Ser Ser	Leu Ser Ser Leu Gly	Glu		
	755	760	765		
Asp Gln Asp Ser	Val Leu Thr Pro Glu	Glu Val Ala Leu Cys	Leu		
	770	775	780		
Glu Leu Ser Glu	Gly Glu Glu Thr Pro	Arg Asn Ser Val Ser	Pro		
	785	790	795		
Met Pro Arg Ala	Pro Ser Pro Pro Thr	Thr Tyr Gly Tyr Ile	Ser		
	800	805	810		
Val Pro Thr Ala	Ser Glu Phe Thr Asp	Met Gly Arg Thr Gly	Gly		
	815	820	825		

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 214

aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<210> 215

<211> 2749

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1869, 1887

<223> unknown base

<400> 215

ctcccacggt gtccagcgcc cagaatgcgg cttctgggtcc tgctatgggg 50

ttgcctgctg ctcccagggt atgaagccct ggagggccca gaggaaatca 100

gcggggttca aggggacact gtgtccctgc agtgcaccta cagggaagag 150

ctgagggacc accggaagta ctgggtgcagg aaggggtggga tcctcttctc 200

tcgctgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250

agggcaggggt gtccatccgt gacagccgcc aggagctctc gctcattgtg 300

accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtgggggt 350

cgaaaaacgg ggccccgatg agtctttact gatctctctg ttogtctttc 400

caggaccctg ctgtcctccc tccccttctc ccaccttcca gcctctgggt 450

acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agccccaggg 500

attgacttct cctgggctct acccggcagc caccacagcc aagcagggga 550

agacaggggc tgaggccctt ccattgccag ggacttccca gtacggggcac 600

gaaaggactt ctcagtacac aggaacctct cctcaccag cgacctctcc 650

tcctgcaggg agctcccgcc ccccatgca gctggactcc acctcagcag 700

aggacaccag tccagctctc agcagtggca gctctaagcc cagggtgtcc 750

atcccgatgg tccgcatact ggccccagtc ctgggtgctg tgagccttct 800

gtcagccgca ggcctgatcg cttctgcag ccacctgctc ctgtggagaa 850

aggaagctca acaggccacg gagacacaga ggaacgagaa gttctggctc 900

tcacgcttga ctgcggagga aaaggaagcc ccttcccagg cccctgaggg 950

ggacgtgatc tcgatgcctc ccctccacac atctgaggag gagctggggt 1000

tctcgaagtt	tgtctcagcg	tagggcagga	ggccctcctg	gccaggccag	1050
cagtgaagca	gtatggctgg	ctggatcagc	accgattccc	gaaagctttc	1100
cacctcagcc	tcagagtcca	gctgcccgga	ctccagggct	ctccccaccc	1150
tccccaggct	ctcctcttgc	atgttccagc	ctgacctaga	agcgtttgtc	1200
agccctggag	cccagagcgg	tggccttgct	cttccggctg	gagactggga	1250
catccctgat	aggttcacat	ccctgggcag	agtaccaggc	tgctgaccct	1300
cagcagggcc	agacaaggct	cagtggatct	ggtctgagtt	tcaatctgcc	1350
aggaactcct	gggcctcatg	cccagtgtcg	gaccctgcct	tcctcccact	1400
ccagacccca	ccttgtcttc	cctccctggc	gtcctcagac	ttagtcccac	1450
ggtctcctgc	atcagctggg	gatgaagagg	agcatgctgg	ggtgagactg	1500
ggattctggc	ttctctttga	accacctgca	tccagccctt	caggaagcct	1550
gtgaaaaacg	tgattcctgg	ccccaccaag	acccaccaa	accatctctg	1600
ggcttggtgc	aggactctga	attctaaca	tgcccagtga	ctgtcgcact	1650
tgagtttgag	ggccagtg	cctgatgaac	gctcacaccc	cttcagctta	1700
gagtctgcat	ttgggctgtg	acgtctccac	ctgccccaat	agatctgctc	1750
tgtctgcgac	accagatcca	cgtggggact	cccctgaggc	ctgctaagtc	1800
caggccttgg	tcaggtcagg	tgcacattgc	aggataagcc	caggaccggc	1850
acagaagtgg	ttgcctttnc	catttgccct	ccctggncca	tgctttcttg	1900
cctttggaaa	aatgatgaa	gaaaaccttg	gctccttcct	tgtctggaaa	1950
gggttacttg	cctatgggtt	ctgggtggcta	gagagaaaag	tagaaaacca	2000
gagtgcacgt	aggtgtctaa	cacagaggag	agtaggaaca	gggcgatac	2050
ctgaaggtga	ctccgagtcc	agccccctgg	agaaggggtc	gggggtggtg	2100
gtaaagtagc	acaactacta	ttttttttct	ttttccatta	ttattgtttt	2150
ttaagacaga	atctcgtgct	gctgcccagg	ctggagtgca	gtggcacgat	2200
ctgcaaactc	cgcctcctgg	gttcaagtga	ttctttctgcc	tcagcctccc	2250
gagtagctgg	gattacaggc	acgcaccacc	acacctggct	aatttttgta	2300
cttttagtag	agatgggggtt	tcaccatgtt	ggccaggctg	gtcttgaact	2350
cctgacctca	aatgagcctc	ctgcttcagt	ctcccaaatt	gccgggatta	2400
caggcatgag	ccactgtgtc	tggccctatt	tccttttaaaa	agtgaaatta	2450

agagttgttc agtatgcaaa acttggaag atggaggaga aaaagaaaag 2500
 gaagaaaaaa atgtcaccca tagtctcacc agagactatc attatttcgt 2550
 tttgtgttac ttccctccac tcttttcttc ttcacataat ttgccggtgt 2600
 tctttttaca gagcaattat cttgtatata caactttgta tcctgccttt 2650
 tccaccttat cgttccatca ctttattcca gcacttctct gtgttttaca 2700
 gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaaa 2749

<210> 216
 <211> 332
 <212> PRT
 <213> Homo sapiens

<400> 216
 Met Arg Leu Leu Val Leu Leu Trp Gly Cys Leu Leu Leu Pro Gly
 1 5 10 15
 Tyr Glu Ala Leu Glu Gly Pro Glu Glu Ile Ser Gly Phe Glu Gly
 20 25 30
 Asp Thr Val Ser Leu Gln Cys Thr Tyr Arg Glu Glu Leu Arg Asp
 35 40 45
 His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg
 50 55 60
 Cys Ser Gly Thr Ile Tyr Ala Glu Glu Gly Gln Glu Thr Met
 65 70 75
 Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu
 80 85 90
 Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr
 95 100 105
 Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile
 110 115 120
 Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser
 125 130 135
 Pro Thr Phe Gln Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala
 140 145 150
 Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu
 155 160 165
 Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu
 170 175 180
 Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr
 185 190 195
 Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro

	200	205	210
Ala Gly Ser Ser	Arg Pro Pro Met Gln	Leu Asp Ser Thr Ser	Ala
	215	220	225
Glu Asp Thr Ser	Pro Ala Leu Ser Ser	Gly Ser Ser Lys Pro	Arg
	230	235	240
Val Ser Ile Pro	Met Val Arg Ile Leu	Ala Pro Val Leu Val	Leu
	245	250	255
Leu Ser Leu Leu	Ser Ala Ala Gly Leu	Ile Ala Phe Cys Ser	His
	260	265	270
Leu Leu Leu Trp	Arg Lys Glu Ala Gln	Gln Ala Thr Glu Thr	Gln
	275	280	285
Arg Asn Glu Lys	Phe Trp Leu Ser Arg	Leu Thr Ala Glu Glu	Lys
	290	295	300
Glu Ala Pro Ser	Gln Ala Pro Glu Gly	Asp Val Ile Ser Met	Pro
	305	310	315
Pro Leu His Thr	Ser Glu Glu Glu Leu	Gly Phe Ser Lys Phe	Val
	320	325	330
Ser Ala			

<210> 217

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 217

ccctgcagtg cacctacagg gaag 24

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 218

ctgtcttccc ctgcttggct gtgg 24

<210> 219

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 219

ggtgcaggaa ggtggtgatc ctcttctctc gctgctctgg ccacatc 47

<210> 220

<211> 950

<212> DNA

<213> Homo sapiens

<400> 220

ttgtgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50
ggggtggcag gagccgcaga gccagagcag acagccgaga aacagggtga 100
cagtgtgaaa gaaccagtgg tctcgctctg ttgccagggc tagagtgtac 150
tggcgtgatc atagctcact gcagcctcag actcctggac ttgagaaatc 200
ctcctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250
cctgtttctt ctcttctgt gagtggacca cggaggctgg tgagctgcct 300
gtcatcccaa agctcagctc tgagccagag tgggtggtggc tccacctctg 350
ccgccggcat agaagccagg agcagggtc tcagaaggcg gtggtgccca 400
gctgggatca tgttgttggc cctggtctgt ctgctcagct gcctgctacc 450
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ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650
ggtgcagcaa cctcaccocg aacgtcccca acgtgtgccg gatgtactgc 700
tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750
gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800
actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850
gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900
cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221

<211> 146

<212> PRT

<213> Homo sapiens

<400> 221

Met	Leu	Leu	Ala	Leu	Val	Cys	Leu	Leu	Ser	Cys	Leu	Leu	Pro	Ser
1				5					10					15
Ser	Glu	Ala	Lys	Leu	Tyr	Gly	Arg	Cys	Glu	Leu	Ala	Arg	Val	Leu
				20					25					30

His	Asp	Phe	Gly	Leu	Asp	Gly	Tyr	Arg	Gly	Tyr	Ser	Leu	Ala	Asp
				35					40					45
Trp	Val	Cys	Leu	Ala	Tyr	Phe	Thr	Ser	Gly	Phe	Asn	Ala	Ala	Ala
				50					55					60
Leu	Asp	Tyr	Glu	Ala	Asp	Gly	Ser	Thr	Asn	Asn	Gly	Ile	Phe	Gln
				65					70					75
Ile	Asn	Ser	Arg	Arg	Trp	Cys	Ser	Asn	Leu	Thr	Pro	Asn	Val	Pro
				80					85					90
Asn	Val	Cys	Arg	Met	Tyr	Cys	Ser	Asp	Leu	Leu	Asn	Pro	Asn	Leu
				95					100					105
Lys	Asp	Thr	Val	Ile	Cys	Ala	Met	Lys	Ile	Thr	Gln	Glu	Pro	Gln
				110					115					120
Gly	Leu	Gly	Tyr	Trp	Glu	Ala	Trp	Arg	His	His	Cys	Gln	Gly	Lys
				125					130					135
Asp	Leu	Thr	Glu	Trp	Val	Asp	Gly	Cys	Asp	Phe				
				140					145					

<210> 222

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 222

gggatcatgt tggtagccct ggtc 24

<210> 223

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 223

gcaaggcaga cccagtcagc cag 23

<210> 224

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 224

ctgcctgcta ccctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225

<211> 2049
<212> DNA
<213> Homo sapiens

<400> 225
agccgctgcc ccggggccggg cggccgcggc ggcacccatga gtccccgctc 50
gtgcctgcgt tcgctgcgcc tcctcgtctt cgccgtcttc tcagccgccg 100
cgagcaactg gctgtacctg gccaaagctgt cgtcgggtggg gagcatctca 150
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200
gatgtgcaag cggaacctgg aagtcattga ctccgtgcgc ccggtgccc 250
agctggccat tgaggagtgc cagtaccagt tccggaaccg gcgctggaac 300
tgctccacac tcgactcctt gcccgctctt ggcaaggtgg tgacgcaagg 350
gactcgggag gcggccttcg tgtacgcat ctcttcggca ggtgtggcct 400
ttgcagtgac gcgggcgtgc agcagtggg agctggagaa gtgcggctgt 450
gacaggacag tgcattgggt cagcccacag ggcttcacgt ggtcaggatg 500
ctctgacaac atcgccctac gtgtggcctt ctacagtcg tttgtggatg 550
tgccggagag aagcaagggg gcctcgtcca gcagagccct catgaacctc 600
cacaacaatg aggccggcag gaaggccatc ctgacacaca tgcgggtgga 650
atgcaagtgc caggggtgt caggctcctg tgaggtaaag acgtgctggc 700
gagccgtgcc gcccttcgc cagggtgggtc acgcactgaa ggagaagttt 750
gatggtgcca ctgagggtga gccacgccgc gtgggctcct ccagggcact 800
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ctgggcacga ggggccgcac atgcaacaag acgtccaagg ccatcgacgg 950
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cggcagtgcc agcggctcgt ggagttgcac acgtgccgat gaccgcctgc 1100
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aaacagtctc ccaccaccta cccaagaga tactggttgt attttttgtt 1200
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gctgccactg accactcagt tgttatctgt gtccgttttt ctacttgacg 1400
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ccctgagaaa gggaacaagc agataccagg tcaagggcac caggttcatt 1650
tcagccctta catggacagc tagaggttcg atatctgtgg gtccttccag 1700
gcaagaagag ggagatgaga gcaagagacg actgaagtcc caccctagaa 1750
cccagcctgc cccagcctgc ccttggaag aggaaactta accactcccc 1800
agaccacact aggcaggcat ataggctgcc atcctggacc agggatcccc 1850
gctgtgcctt tgcagtcag cccgagtcac ctttcacagc gctgttcctc 1900
catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950
acacacacac ggacacacac acacacctgc gagagagagg gaggaagg 2000
ctgtgccttt gcagtcagc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226

<211> 351

<212> PRT

<213> Homo sapiens

<400> 226

Met	Ser	Pro	Arg	Ser	Cys	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Val	Phe
1				5					10					15
Ala	Val	Phe	Ser	Ala	Ala	Ala	Ser	Asn	Trp	Leu	Tyr	Leu	Ala	Lys
				20					25					30
Leu	Ser	Ser	Val	Gly	Ser	Ile	Ser	Glu	Glu	Glu	Thr	Cys	Glu	Lys
				35					40					45
Leu	Lys	Gly	Leu	Ile	Gln	Arg	Gln	Val	Gln	Met	Cys	Lys	Arg	Asn
				50					55					60
Leu	Glu	Val	Met	Asp	Ser	Val	Arg	Arg	Gly	Ala	Gln	Leu	Ala	Ile
				65					70					75
Glu	Glu	Cys	Gln	Tyr	Gln	Phe	Arg	Asn	Arg	Arg	Trp	Asn	Cys	Ser
				80					85					90
Thr	Leu	Asp	Ser	Leu	Pro	Val	Phe	Gly	Lys	Val	Val	Thr	Gln	Gly
				95					100					105
Thr	Arg	Glu	Ala	Ala	Phe	Val	Tyr	Ala	Ile	Ser	Ser	Ala	Gly	Val
				110					115					120

Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys
				125					130					135
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe
				140					145					150
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe
				155					160					165
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser
				170					175					180
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg
				185					190					195
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly
				200					205					210
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro
				215					220					225
Pro	Phe	Arg	Gln	Val	Gly	His	Ala	Leu	Lys	Glu	Lys	Phe	Asp	Gly
				230					235					240
Ala	Thr	Glu	Val	Glu	Pro	Arg	Arg	Val	Gly	Ser	Ser	Arg	Ala	Leu
				245					250					255
Val	Pro	Arg	Asn	Ala	Gln	Phe	Lys	Pro	His	Thr	Asp	Glu	Asp	Leu
				260					265					270
Val	Tyr	Leu	Glu	Pro	Ser	Pro	Asp	Phe	Cys	Glu	Gln	Asp	Met	Arg
				275					280					285
Ser	Gly	Val	Leu	Gly	Thr	Arg	Gly	Arg	Thr	Cys	Asn	Lys	Thr	Ser
				290					295					300
Lys	Ala	Ile	Asp	Gly	Cys	Glu	Leu	Leu	Cys	Cys	Gly	Arg	Gly	Phe
				305					310					315
His	Thr	Ala	Gln	Val	Glu	Leu	Ala	Glu	Arg	Cys	Ser	Cys	Lys	Phe
				320					325					330
His	Trp	Cys	Cys	Phe	Val	Lys	Cys	Arg	Gln	Cys	Gln	Arg	Leu	Val
				335					340					345
Glu	Leu	His	Thr	Cys	Arg									
				350										

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaattccac tgg 23

<210> 228
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 228
tgggtgggaga ctgttttaa at tatcggcc 28

<210> 229
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 229
tgcttcgtca agtgccggca gtgccagcgg ctcgtggagt t 41

<210> 230
<211> 1355
<212> DNA
<213> Homo sapiens

<400> 230
cggacgcgtg ggcggacgcg tgggcgacgc cgtgggcgga cgcgtgggct 50
gggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcggca 100
gctccgagga ggtccccgga gggccctggg gacgctgggt gcaactggagc 150
aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcctttg 200
ggctgtgatt ctgagtatcc tattgtccaa ggcctccacg gaggcgcgcg 250
cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300
gcggcgctgg gtgccctgaa ggaggaggtc ggagactgcc acagctgctg 350
ctcggggacg caggcgcagc tgcagaccac gcgcgcggag cttggggagg 400
cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450
cgcgtgacct agggcttggc tgaagccggc aggggccgtg aggacgtccg 500
cactgagctg ttccggggcg tggaggccgt gaggtccag aacaactcct 550
gcgagccgtg cccacgtcg tggctgtcct tcgagggctc ctgctacttt 600
ttctctgtgc caaagacgac gtgggcggcg gcgcaggatc actgcgcaga 650
tgccagcgcg cacctggtga tcgttggggg cctggatgag cagggttcc 700
tcactcgga cagcgtggc cgtggttact ggctgggcct gagggctgtg 750

cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800
cagcttcagc cactggaacc agggagagcc caatgacgct tgggggcgcg 850
agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900
gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950
cogcccagtg ccctggagcc gcgcccattg cagcatgtcg tatcctgggg 1000
gctgctcacc tccctggctc ctggagctga ttgccaaaga gtttttttct 1050
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tgtccagccc agtgccctggg ctctgggacc tccatgccga cctcatccta 1150
actccactca cgcagaccca acctaacctc cactagctcc aaaatccctg 1200
ctoctgcgtc cccgtgatat gcctccactt ctctccctaa ccaaggttag 1250
gtgactgagg actggagctg tttggttttc tcgcattttc caccaaactg 1300
gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350
aaaaa 1355

<210> 231
<211> 293
<212> PRT
<213> Homo sapiens

<400> 231
Met Asp Thr Thr Arg Tyr Ser Lys Trp Gly Gly Ser Ser Glu Glu
1 5 10 15
Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg
20 25 30
Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp
35 40 45
Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg
50 55 60
Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser
65 70 75
Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp
80 85 90
Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr
95 100 105
Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu
110 115 120
Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala
125 130 135

Glu	Ala	Gly	Arg	Gly	Arg	Glu	Asp	Val	Arg	Thr	Glu	Leu	Phe	Arg	
				140					145					150	
Ala	Leu	Glu	Ala	Val	Arg	Leu	Gln	Asn	Asn	Ser	Cys	Glu	Pro	Cys	
				155					160					165	
Pro	Thr	Ser	Trp	Leu	Ser	Phe	Glu	Gly	Ser	Cys	Tyr	Phe	Phe	Ser	
				170					175					180	
Val	Pro	Lys	Thr	Thr	Trp	Ala	Ala	Ala	Gln	Asp	His	Cys	Ala	Asp	
				185					190					195	
Ala	Ser	Ala	His	Leu	Val	Ile	Val	Gly	Gly	Leu	Asp	Glu	Gln	Gly	
				200					205					210	
Phe	Leu	Thr	Arg	Asn	Thr	Arg	Gly	Arg	Gly	Tyr	Trp	Leu	Gly	Leu	
				215					220					225	
Arg	Ala	Val	Arg	His	Leu	Gly	Lys	Val	Gln	Gly	Tyr	Gln	Trp	Val	
				230					235					240	
Asp	Gly	Val	Ser	Leu	Ser	Phe	Ser	His	Trp	Asn	Gln	Gly	Glu	Pro	
				245					250					255	
Asn	Asp	Ala	Trp	Gly	Arg	Glu	Asn	Cys	Val	Met	Met	Leu	His	Thr	
				260					265					270	
Gly	Leu	Trp	Asn	Asp	Ala	Pro	Cys	Asp	Ser	Glu	Lys	Asp	Gly	Trp	
				275					280					285	
Ile	Cys	Glu	Lys	Arg	His	Asn	Cys								
				290											

<210> 232
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 232
 gcgagaactg tgtcatgatg ctgc 24

 <210> 233
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 233
 gtttctgaga ctcagcagcg gtgg 24

 <210> 234
 <211> 50
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

gccaggggaa gagggatgatc cgacccgggg aaggtcgctg ggcagggcga 50

gttgggaaag cggcagcccc cgccgcccc gcagcccctt ctctctcttt 100

ctcccacgtc ctatctgcct ctcgctggag gccaggccgt gcagcatcga 150

agacaggagg aactggagcc tcattggccg gcccgggcg ccggcctcgg 200

gcttaaataag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250

cgctcccgt gtcctgccg ggtgatggaa aacccagcc cggccgccgc 300

cctgggcaag gccctctgcg ctctctcct ggccactctc ggcgccgccg 350

gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400

tacagcatca ccttcacggg caagtggagc cagacggcct tccccagca 450

gtaccccctg ttccgcccc ctgcgcagtg gtcttcgctg ctggggggccg 500

cgcatagctc cgactacagc atgtggagga agaaccagta cgtcagtaac 550

gggctgcgcg actttgcgga gcgcggcgag gcctgggcgc tgatgaagga 600

gatcgaggcg gcgggggagg cgctgcagag cgtgcacgag gtgttttcgg 650

cgcccgccgt cccagcggc accgggcaga cgtcggcgga gctggagggtg 700

cagcgcaggc actcgctggt ctcgtttggt gtgcgcacgt tgcccagccc 750

cgactggttc gtgggcgtgg acagcctgga cctgtgcgac ggggaccgtt 800

ggcgggaaca ggcggcgctg gacctgtacc cctacgacgc cgggacggac 850

agcggcttca ctttctctc ccccaacttc gccaccatcc cgcaggacac 900

ggtgaccgag ataacgtcct cctctcccag ccaccggcc aactccttct 950

actacccgcg gctgaaggcc ctgcctcca tcgccagggt gacactgctg 1000

cggctgcgac agagccccag ggccttcac cctcccgcc cagtctgcc 1050

cagcagggac aatgagattg tagacagcgc ctcagttcca gaaacgccgc 1100

tggactgcga ggtctccctg tggctcgtcct ggggactgtg cggaggccac 1150
 tgtgggagggc tcgggaccaa gagcaggact cgctacgtcc ggggccagcc 1200
 cgccaacaac gggagcccct gccccgagct cgaagaagag gctgagtgcg 1250
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 cggagccatg ggggtgtcggg ggctcctgtg caggctcatg ctgcaggcgg 1350
 ccgagggcac aggggggtttc gcgctgctcc tgaccgcggt gaggccgcgc 1400
 cgaccatctc tgcactgaag ggccctctgg tggccggcac gggcattggg 1450
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 gtctgtctc agcctcctcc tcctgcagga taaagtcac cccaaggctc 1550
 cagctactct aaattatgtc tccttataag ttattgctgc tccaggagat 1600
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 gacctggtgc tctaggctgt gctgagccca ctctcccag ggcgcatcca 1700
 agcggggggc acttgagaag tgaataaatg gggcggtttc ggaagcgtca 1750
 gtgtttccat gttatggatc tctctgcgtt tgaataaaga ctatctctgt 1800
 tgotcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236

<211> 331

<212> PRT

<213> Homo sapiens

<400> 236

Met	Glu	Asn	Pro	Ser	Pro	Ala	Ala	Ala	Leu	Gly	Lys	Ala	Leu	Cys
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Ala	Leu	Leu	Leu	Ala	Thr	Leu	Gly	Ala	Ala	Gly	Gln	Pro	Leu	Gly
				20					25					30
Gly	Glu	Ser	Ile	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Lys	Tyr	Ser	Ile
				35					40					45
Thr	Phe	Thr	Gly	Lys	Trp	Ser	Gln	Thr	Ala	Phe	Pro	Lys	Gln	Tyr
				50					55					60
Pro	Leu	Phe	Arg	Pro	Pro	Ala	Gln	Trp	Ser	Ser	Leu	Leu	Gly	Ala
				65					70					75
Ala	His	Ser	Ser	Asp	Tyr	Ser	Met	Trp	Arg	Lys	Asn	Gln	Tyr	Val
				80					85					90
Ser	Asn	Gly	Leu	Arg	Asp	Phe	Ala	Glu	Arg	Gly	Glu	Ala	Trp	Ala
				95					100					105
Leu	Met	Lys	Glu	Ile	Glu	Ala	Ala	Gly	Glu	Ala	Leu	Gln	Ser	Val

<210> 238
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 238
caggactcgc tacgtccg 18

<210> 239
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 239
cagcccccttc tcctcctttc tccc 24

<210> 240
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 240
gcagttatca gggacgcact cagcc 25

<210> 241
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 241
ccagcgagag gcagatag 18

<210> 242
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 242
cggtcaccgt gtctgcggg atg 23

<210> 243
<211> 42
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 243

cagcccccttc tcctcctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894

<212> DNA

<213> Homo sapiens

<400> 244

ggcggcgtcc gtgagggggt cctttgggca ggggtagtgt ttggtgtccc 50
tgtcttgctg gatattgaca aactgaagct ttctgcacc actggactta 100
aggaagagtg tactcgtagg cggacagctt tagtggccgg ccggccgctc 150
tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250
gctggagata ttgacataga gttgtggtcc aaagaagctc ctaaagcttg 300
cagaaatfff atccaactff gtttgaagc ttattatgac aataccatff 350
ttcatagagt tgtgcctggt ttcatagtcc aaggcggaga tcctactggc 400
acagggagtg gtggagagtc tatctatgga gcgccattca aagatgaatt 450
tcattcacgg ttgcgtffta atcgagagg actggttgcc atggcaaatg 500
ctggtttctca tgataatggc agccagttff tcttcacact gggtcgagca 550
gatgaactta acaataagca taccatctff ggaaaggffa caggggatac 600
agtatataac atgttgcgac tgtcagaagt agacattgat gatgacgaaa 650
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tttgatgaca tcattccaag ggaaattaaa aggctgaaaa aagagaaacc 750
agaggaggaa gtaaagaaat tgaaacccaa aggcacaaaa aatffftagtt 800
tactfftcatt tggagaggaa gctgaggaag aagaggagga agtaaatcga 850
gttagtcaga gcatgaaggg caaaagcaaa agtagtcatg acttgcttaa 900
ggatgatcca catctcagtt ctgttccagt thtagaaagt gaaaaagggtg 950
atgcaccaga tfftagttgat gatggagaag atgaaagtgc agagcatgat 1000
gaatatattg atggtgatga aaagaacctg atgagagaaa gaattgccaa 1050
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aagtggagaa gaaatcagtc agccgcagtg aagagctcag aaaagaagca 1150
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tgcagcaaaa caagcagaaa aaagaagtga agaggaagaa gcccctccag 1250
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ctgaaaatga cattcctgaa acagaagtag aagatgatga aggatggatg 1450
tcacatgtac ttcagtttga ggataaaagc agaaaagtga aagatgcaag 1500
catgcaagac tcagatacat ttgaaatcta tgatcctcgg aatccagtga 1550
ataaaaagaag gaggggaagaa agcaaaaagc tgatgagaga gaaaaaagaa 1600
agaagataaa atgagaataa tgataaccag aacttgctgg aaatgtgcct 1650
acaatggcct tgtaacagcc attgttccca acagcatcac ttaggggtgt 1700
gaaaagaagt atttttgaac ctgttgtctg gttttgaaaa acaattatct 1750
tgttttgcaa attgtggaat gatgtaagca aatgcttttg gttactggta 1800
catgtgtttt ttcctagctg accttttata ttgctaaatc tgaaataaaa 1850
taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245

<211> 472

<212> PRT

<213> Homo sapiens

<400> 245

Met	Ser	Asn	Ile	Tyr	Ile	Gln	Glu	Pro	Pro	Thr	Asn	Gly	Lys	Val
1				5					10					15

Leu	Leu	Lys	Thr	Thr	Ala	Gly	Asp	Ile	Asp	Ile	Glu	Leu	Trp	Ser
			20					25						30

Lys	Glu	Ala	Pro	Lys	Ala	Cys	Arg	Asn	Phe	Ile	Gln	Leu	Cys	Leu
			35					40						45

Glu	Ala	Tyr	Tyr	Asp	Asn	Thr	Ile	Phe	His	Arg	Val	Val	Pro	Gly
			50					55						60

Phe	Ile	Val	Gln	Gly	Gly	Asp	Pro	Thr	Gly	Thr	Gly	Ser	Gly	Gly
			65					70						75

Glu	Ser	Ile	Tyr	Gly	Ala	Pro	Phe	Lys	Asp	Glu	Phe	His	Ser	Arg
			80					85						90

Leu	Arg	Phe	Asn	Arg	Arg	Gly	Leu	Val	Ala	Met	Ala	Asn	Ala	Gly
			95					100						105

Ser His Asp Asn Gly Ser Gln Phe Phe Phe Thr Leu Gly Arg Ala	110	115	120
Asp Glu Leu Asn Asn Lys His Thr Ile Phe Gly Lys Val Thr Gly	125	130	135
Asp Thr Val Tyr Asn Met Leu Arg Leu Ser Glu Val Asp Ile Asp	140	145	150
Asp Asp Glu Arg Pro His Asn Pro His Lys Ile Lys Ser Cys Glu	155	160	165
Val Leu Phe Asn Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys	170	175	180
Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys	185	190	195
Pro Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu	200	205	210
Ala Glu Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met	215	220	225
Lys Gly Lys Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro	230	235	240
His Leu Ser Ser Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala	245	250	255
Pro Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp	260	265	270
Glu Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile	275	280	285
Ala Lys Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala	290	295	300
Gly Glu Gly Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu	305	310	315
Leu Arg Lys Glu Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala	320	325	330
Lys Gln Lys Lys Val Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg	335	340	345
Ser Glu Glu Glu Glu Ala Pro Pro Asp Gly Ala Val Ala Glu Tyr	350	355	360
Arg Arg Glu Lys Gln Lys Tyr Glu Ala Leu Arg Lys Gln Gln Ser	365	370	375
Lys Lys Gly Thr Ser Arg Glu Asp Gln Thr Leu Ala Leu Leu Asn	380	385	390
Gln Phe Lys Ser Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro Glu			

	395		400		405
Asn Asp Ile Pro	Glu Thr Glu Val Glu	Asp Asp Glu Gly Trp	Met		
	410	415	420		
Ser His Val Leu	Gln Phe Glu Asp Lys	Ser Arg Lys Val Lys	Asp		
	425	430	435		
Ala Ser Met Gln	Asp Ser Asp Thr Phe	Glu Ile Tyr Asp Pro	Arg		
	440	445	450		
Asn Pro Val Asn	Lys Arg Arg Arg Glu	Glu Ser Lys Lys Leu	Met		
	455	460	465		
Arg Glu Lys Lys	Glu Arg Arg				
	470				

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

tgcgagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

cgagttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 248

cagatggtgc tgttgccg 18

<210> 249

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 249
caactggaac aggaactgag atgtggatc 29

<210> 250

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 250

ctggttcagc agtgaaggg tctg 24

<210> 251

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 251

cctctccgat taaaacgc 18

<210> 252

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 252

gagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45

<210> 253

<211> 2456

<212> DNA

<213> Homo sapiens

<400> 253

cgccgccgtt ggggctggaa gttcccgcga ggtccgtgcc gggcgagaga 50

gatgctgccc ggccgcctc ggctttgagg cgagagaagt gtcccagacc 100

catttcgcct tgctgacggc gtcgagccct ggccagacat gtccacaggg 150

ttctccttcg ggtccgggac tctgggctcc accaccgtgg ccgccggcgg 200

gaccagcaca ggcggcggtt tctccttcgg aacgggaacg tctagcaacc 250

cttctgtggg gctcaatttt ggaaatcttg gaagtacttc aactccagca 300

actacatctg ctcttcaag tggttttgga accgggctct ttggatctaa 350

acctgccact gggttcactc taggaggaac aaatacaggt gccttgaca 400

ccaagaggcc tcaagtggtc accaaatatg gaaccctgca aggaaaacag 450
 atgcatgtgg ggaagacacc catccaagtc tttttaggag tccccttctc 500
 cagacctcct ctaggatatcc tcaggtttgc acctccagaa cccccggagc 550
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 ctccgcctcc cgggttcaag cgagtotoct gcctcagcct ctgagtgtct 700
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 gtcagcacgc gggaacggta caagtggctg cgcttcagcg aggactgtct 800
 gtacctgaac gtgtacgcgc cggcgcgcg gcgcggggat cccagctgc 850
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 tgcccacctg gctggatgca accacaacag cacacagatc ctggtaaact 1300
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 agattcctcc aactgaactt ccagagagac ccggaagaga ttatctggtc 1400
 catgagccct gtggtggatg gtgtggtgat cccagatgac cctttggtgc 1450
 tcctgacca ggggaaggtt tcactgtgtc cctaccttct aggtgtcaac 1500
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 agatgctacg aaaccgtatg atggacatag ttcaagatgc cactttcgtg 1650
 tatgccacac tgcagactgc tctactaccac cgagaaaccc caatgatggg 1700
 aatctgccct gctggccacg ctacaacaag gatgaaaagt acctgcagct 1750
 ggattttacc acaagagtgg gcatgaagct caaggagaag aagatggctt 1800
 tttgatgag tctgtaccag tctcaaagac ctgagaagca gaggcaattc 1850

taagggtggc tatgcaggaa ggagccaaag aggggtttgc ccccaaccatc 1900
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 ccaccccagt ttagaactgc aggagctccc tgctgcctcc aggccaaagc 2000
 tagagctttt gcctgtgtg tgggacctgc actgcccttt ccagcctgac 2050
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 ctgtcaacac cacactgtgc tcagctctcc agcctcagga caacctcttt 2150
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 cttggcattt accatccatc ctgctcaacc ttgttctgt ctgttcacat 2300
 tggcctggag gcctagggca ggttgtgaca tggagcaaac ttttggtagt 2350
 ttgggatctt ctctcccacc cacacttata tccccaggg ccactccaaa 2400
 gtctatacac aggggtgggc tcttcaataa agaagtgttg attagaaaaa 2450
 aaaaaa 2456

<210> 254
 <211> 545
 <212> PRT
 <213> Homo sapiens

<400> 254
 Met Ser Thr Gly Phe Ser Phe Gly Ser Gly Thr Leu Gly Ser Thr
 1 5 10 15
 Thr Val Ala Ala Gly Gly Thr Ser Thr Gly Gly Val Phe Ser Phe
 20 25 30
 Gly Thr Gly Thr Ser Ser Asn Pro Ser Val Gly Leu Asn Phe Gly
 35 40 45
 Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser
 50 55 60
 Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly
 65 70 75
 Phe Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg
 80 85 90
 Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met
 95 100 105
 His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe
 110 115 120
 Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro
 125 130 135

Pro	Glu	Pro	Trp	Lys	Gly	Ile	Arg	Asp	Ala	Thr	Thr	Tyr	Pro	Pro	140	145	150
Gly	Trp	Ser	Leu	Ala	Leu	Ser	Pro	Gly	Trp	Ser	Ala	Val	Ala	Arg	155	160	165
Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ala	Ser	Arg	Val	Gln	Ala	Ser	Leu	170	175	180
Leu	Pro	Gln	Pro	Leu	Ser	Val	Trp	Gly	Tyr	Arg	Cys	Leu	Gln	Glu	185	190	195
Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg	Glu	Arg	200	205	210
Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	215	220	225
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met	230	235	240
Val	Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser	245	250	255
Tyr	Glu	Gly	Ser	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Val	Val	Leu	Val	260	265	270
Phe	Leu	Gln	His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp	275	280	285
Asp	Ser	His	Ala	Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala	290	295	300
Ala	Leu	Arg	Trp	Val	Gln	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	305	310	315
Pro	Gly	Asn	Val	Thr	Leu	Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser	320	325	330
Ile	Ser	Gly	Leu	Met	Met	Ser	Pro	Leu	Ala	Ser	Gly	Leu	Phe	His	335	340	345
Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr	Ala	Leu	Phe	Arg	Leu	Phe	Ile	350	355	360
Thr	Ser	Asn	Pro	Leu	Lys	Val	Ala	Lys	Lys	Val	Ala	His	Leu	Ala	365	370	375
Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu	Val	Asn	Cys	Leu	Arg	380	385	390
Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val	Ser	Asn	Lys	Met	Arg	395	400	405
Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu	Glu	Ile	Ile	Trp	410	415	420
Ser	Met	Ser	Pro	Val	Val	Asp	Gly	Val	Val	Ile	Pro	Asp	Asp	Pro			

425	430	435
Leu Val Leu Leu Thr Gln Gly Lys Val	Ser Ser Val Pro Tyr Leu	
440	445	450
Leu Gly Val Asn Asn Leu Glu Phe Asn	Trp Leu Leu Pro Tyr Asn	
455	460	465
Ile Thr Lys Glu Gln Val Pro Leu Val	Val Glu Glu Tyr Leu Asp	
470	475	480
Asn Val Asn Glu His Asp Trp Lys Met	Leu Arg Asn Arg Met Met	
485	490	495
Asp Ile Val Gln Asp Ala Thr Phe Val	Tyr Ala Thr Leu Gln Thr	
500	505	510
Ala His Tyr His Arg Glu Thr Pro Met	Met Gly Ile Cys Pro Ala	
515	520	525
Gly His Ala Thr Thr Arg Met Lys Ser	Thr Cys Ser Trp Ile Leu	
530	535	540
Pro Gln Glu Trp Ala		
545		

<210> 255

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 255

aggtgcctgc aggagtcctg ggg 23

<210> 256

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 256

ccacctcagg aagccgaaga tgcc 24

<210> 257

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 257

gaacgtaca agtggctgcy cttcagcgag gactgtctgt acctg 45

<210> 258
<211> 2764
<212> DNA
<213> Homo sapiens

<400> 258
gagaacaggc ctgtctcagg caggccctgc gcctcctatg cggagatgct 50
actgccactg ctgctgtcct cgctgctggg cgggtcccag gctatggatg 100
ggagattctg gatacgagtg caggagtcag tgatggtgcc ggagggcctg 150
tgcattctctg tgccctgctc tttctcctac ccccgacaag actggacagg 200
gtctacccca gcttatggct actggttcaa agcagtgaact gagacaacca 250
agggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300
acccggggcc gattccagct cactggggat cccgccaagg ggaactgctc 350
cttggtgatc agagacgcgc agatgcagga tgagtcacag tacttctttc 400
gggtggagag aggaagctat gtgacatata atttcatgaa cgatggggtc 450
tttctaaaag taacagtgtc cagcttcacg cccagacccc aggaccacaa 500
caccgacctc acctgccatg tggacttctc cagaaagggg gtgagcgcac 550
agaggaccgt ccgactccgt gtggcctatg ccccagaga ccttgttatc 600
agcatttcac gtgacaacac gccagccctg gagccccagc cccagggaaa 650
tgtcccatac ctggaagccc aaaaaggcca gttcctgcgg ctctctgtgtg 700
ctgctgacag ccagccccct gccacactga gctgggtcct gcagaacaga 750
gtcctctcct cgtcccatcc ctggggccct agacccttg ggctggagct 800
gcccggggtg aaggtctggg attcagggcg ctacacctgc cgagcggaga 850
acaggcttgg ctcccagcag cgagccctgg acctctctgt gcagtatcct 900
ccagagaacc tgagagtgat ggtttcccaa gcaaacagga cagtccctgga 950
aaaccttggg aacggcacgt ctctcccagt actggagggc caaagcctgt 1000
gcctggtctg tgtcacacac agcagccccc cagccaggct gagctggacc 1050
cagaggggac aggttctgag cccctcccag ccctcagacc ccggggtcct 1100
ggagctgcct cgggttcaag tggagcacga aggagagttc acctgccacg 1150
ctcggcacc actgggtccc cagcacgtct ctctcagcct ctccgtgcac 1200
tataagaagg gactcatctc aacggcattc tccaacggag cgtttctggg 1250
aatcggcatc acggctcttc ttttctctg cctggccctg atcatcatga 1300

agattctacc gaagagacgg actcagacag aaaccccgag gccaggttc 1350
 tcccggcaca gcacgatcct ggattacatc aatgtggtcc cgacggctgg 1400
 ccccttggtc cagaagcggg atcagaaagc cacaccaaac agtcctcgga 1450
 cccctcctcc accaggtgct cctccccag aatcaaagaa gaaccagaaa 1500
 aagcagtatc agttgccag tttccagaa cccaaatcat ccaactcaagc 1550
 cccagaatcc caggagagcc aagaggagct ccattatgcc acgctcaact 1600
 tcccaggcgt cagaccagc cctgaggccc ggatgcccga gggcaccag 1650
 gcggattatg cagaagtcaa gttccaatga gggctcttta ggcttttagga 1700
 ctgggacttc ggctagggag gaaggtagag taagagggtg aagataacag 1750
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 ctctttctct ctcttttaaa aaaacatctg gccagggcac agtgggtcac 1850
 gcctgtaatc ccagcacttt gggagggtga ggtgggcaga tcgcctgagg 1900
 tcgggagttc gagaccagcc tggccaactt ggtgaaaccc cgtctctact 1950
 aaaaatacaa aaattagctg ggcatggtgg caggcgctg taatcctacc 2000
 tacttgggaa gctgaggcag gagaatcact tgaacctggg agacggaggt 2050
 tgcagtgagc caagatcaca ccattgcacg ccagcctggg caacaaagcg 2100
 agactccatc tcaaaaaaaaa aatcctccaa atgggttggg tgtctgtaat 2150
 ccagcactt tgggaggcta aggtgggtgg attgcttgag ccaggagtt 2200
 cgagaccagc ctgggcaaca tggtgaaacc ccatctctac aaaaaatata 2250
 aaacatagct gggcttggtg gtgtgtgcct gtagtcccag ctgtcagaca 2300
 tttaaaccag agcaactcca tctggaatag gagctgaata aaatgaggct 2350
 gagacctact gggctgcatt ctcagacagt ggaggcattc taagtcacag 2400
 gatgagacag gaggtccgta caagatacag gtcataaaga ctttgctgat 2450
 aaaacagatt gcagtaaaga agccaaccaa atcccaccaa aaccaagttg 2500
 gccacgagag tgacctctgg tgcctctcac tgctacactc ctgacagcac 2550
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 cccaaaaggg ggaggaatga ataatccacc cttgttttag caaataagca 2650
 agaaataacc ataaaagtgg gcaaccagca gctctaggcg ctgctcttgt 2700
 ctatggagta gccattcttt tgttccttta ctttcttaat aaacttgctt 2750

tcaccttaaa aaaa 2764

<210> 259

<211> 544

<212> PRT

<213> Homo sapiens

<400> 259

Met	Leu	Leu	Pro	Leu	Leu	Leu	Ser	Ser	Leu	Leu	Gly	Gly	Ser	Gln	
1				5					10					15	
Ala	Met	Asp	Gly	Arg	Phe	Trp	Ile	Arg	Val	Gln	Glu	Ser	Val	Met	
				20					25					30	
Val	Pro	Glu	Gly	Leu	Cys	Ile	Ser	Val	Pro	Cys	Ser	Phe	Ser	Tyr	
				35					40					45	
Pro	Arg	Gln	Asp	Trp	Thr	Gly	Ser	Thr	Pro	Ala	Tyr	Gly	Tyr	Trp	
				50					55					60	
Phe	Lys	Ala	Val	Thr	Glu	Thr	Thr	Lys	Gly	Ala	Pro	Val	Ala	Thr	
				65					70					75	
Asn	His	Gln	Ser	Arg	Glu	Val	Glu	Met	Ser	Thr	Arg	Gly	Arg	Phe	
				80					85					90	
Gln	Leu	Thr	Gly	Asp	Pro	Ala	Lys	Gly	Asn	Cys	Ser	Leu	Val	Ile	
				95					100					105	
Arg	Asp	Ala	Gln	Met	Gln	Asp	Glu	Ser	Gln	Tyr	Phe	Phe	Arg	Val	
				110					115					120	
Glu	Arg	Gly	Ser	Tyr	Val	Thr	Tyr	Asn	Phe	Met	Asn	Asp	Gly	Phe	
				125					130					135	
Phe	Leu	Lys	Val	Thr	Val	Leu	Ser	Phe	Thr	Pro	Arg	Pro	Gln	Asp	
				140					145					150	
His	Asn	Thr	Asp	Leu	Thr	Cys	His	Val	Asp	Phe	Ser	Arg	Lys	Gly	
				155					160					165	
Val	Ser	Ala	Gln	Arg	Thr	Val	Arg	Leu	Arg	Val	Ala	Tyr	Ala	Pro	
				170					175					180	
Arg	Asp	Leu	Val	Ile	Ser	Ile	Ser	Arg	Asp	Asn	Thr	Pro	Ala	Leu	
				185					190					195	
Glu	Pro	Gln	Pro	Gln	Gly	Asn	Val	Pro	Tyr	Leu	Glu	Ala	Gln	Lys	
				200					205					210	
Gly	Gln	Phe	Leu	Arg	Leu	Leu	Cys	Ala	Ala	Asp	Ser	Gln	Pro	Pro	
				215					220					225	
Ala	Thr	Leu	Ser	Trp	Val	Leu	Gln	Asn	Arg	Val	Leu	Ser	Ser	Ser	
				230					235					240	
His	Pro	Trp	Gly	Pro	Arg	Pro	Leu	Gly	Leu	Glu	Leu	Pro	Gly	Val	
				245					250					255	

<210> 260
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 260
caaagcctgc gcctggctctg tg 22

<210> 261
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 261
ttctggagcc cagaggtgc tgag 24

<210> 262
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 262
ggagctgccca cccattcaaa tggagcacga aggagagttc acctg 45

<210> 263
<211> 2857
<212> DNA
<213> Homo sapiens

<400> 263
tgaagagtaa tagttggaat caaaagagtc aacgcaatga actgttattt 50
actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttggag 100
caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150
ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200
aatgaatacg actagtcac acatcggcca gctaagatct gatttagaca 250
atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300
acttttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350
tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400
tcgctactgg aagggctgtg gaacctgagt ctgagtttgt catcaaagtt 450

tcggatatca atgacaatga accaaaattc ctagatgaac cttatgaggc 500
 cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550
 caagtgatgc tgacgatccc tcaagtggta ataatgctcg tctcctctac 600
 agcttacttc aaggccagcc atatttttct gttgaaccaa caacaggagt 650
 cataagaata tcttctaaaa tggatagaga actgcaagat gagtattggg 700
 taatcattca agccaaggac atgattggtc agccaggagc gttgtctgga 750
 acaacaagtg tattaattaa actttcagat gttaatgaca ataagcctat 800
 atttaaagaa agtttatacc gcttgactgt ctctgaatct gcacccactg 850
 ggacttctat aggaacaatc atggcatatg ataatgacat aggagagaat 900
 gcagaaatgg attacagcat tgaagaggat gattcgcaaa catttgacat 950
 tattactaat catgaaactc aagaaggaat agttatatta aaaaagaaag 1000
 tggattttga gcaccagaac cactacggta ttagagcaaa agttaaaaac 1050
 catcatgttc ctgagcagct catgaagtac cacactgagg cttccaccac 1100
 tttcattaag atccagggtg aagatgttga tgagcctcct cttttcctcc 1150
 ttccatatta tgtatttgaa gtttttgaag aaaccccaca gggatcattt 1200
 gtaggcgtgg tgtctgccac agaccagac aataggaaat ctcctatcag 1250
 gtattctatt actaggagca aagtgttcaa tatcaatgat aatggtacaa 1300
 tcactacaag taactcactg gatcgtgaaa tcagtgcttg gtacaacct 1350
 agtattacag ccacagaaaa atacaatata gaacagatct cttcgatccc 1400
 actgtatgtg caagttctta acatcaatga tcatgctcct gagttctctc 1450
 aatactatga gacttatgtt tgtgaaaatg caggctctgg tcaggtaatt 1500
 cagactatca gtgcagtgga tagagatgaa tccatagaag agcaccattt 1550
 ttactttaat ctatctgtag aagacactaa caattcaagt tttaaatca 1600
 tagataatca agataacaca gctgtcattt tgactaatag aactggtttt 1650
 aaccttcaag aagaacctgt cttctacatc tccatcttaa ttgccgacaa 1700
 tggaatcccg tcacttacia gtacaaacac ccttaccatc catgtctgtg 1750
 actgtggtga cagtgggagc acacagacct gccagtacca ggagcttgtg 1800
 ctttccatgg gattcaagac agaagttatc attgctattc tcatttgcac 1850
 tatgatcata tttgggttta tttttttgac tttgggttta aaacaacgga 1900

gaaaacagat tctatttcct gagaaaagtg aagatttcag agagaatata 1950
 ttccaatatg atgatgaagg ggggtggagaa gaagatacag aggcctttga 2000
 tatagcagag ctgaggagta gtaccataat gcgggaacgc aagactcgga 2050
 aaaccacaag cgctgagatc aggagcctat acaggcagtc tttgcaagtt 2100
 ggccccgaca gtgccatatt caggaaattc attctggaaa agctcgaaga 2150
 agctaatact gatccgtgtg cccctccttt tgattccctc cagacctacg 2200
 cttttgaggg aacaggggtca ttagctggat ccctgagctc cttagaatca 2250
 gcagtctctg atcaggatga aagctatgat taccttaatg agttgggacc 2300
 tcgcttttaa agattagcat gcatgtttgg ttctgcagtg cagtcaaata 2350
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 ttattttaag ctacctacat gctgtcattg aacagagatg tggggagaaa 2550
 tgtaaacaat cagctcacag gcatcaatac aaccagattt gaagtaaaat 2600
 aatgtaggaa gatattaaaa gtagatgaga ggacacaaga tgtagtcgat 2650
 ccttatgcga ttatatcatt atttacttag gaaagagtaa aaataccaaa 2700
 cgagaaaatt taaaggagca aaaatttgca agtcaaatag aaatgtacaa 2750
 atcgagataa catttacatt tctatcatat tgacatgaaa attgaaaatg 2800
 tatagtcaga gaaattttca tgaattattc catgaagtat tgtttccttt 2850
 atttaaa 2857

<210> 264

<211> 772

<212> PRT

<213> Homo sapiens

<400> 264

Met	Asn	Cys	Tyr	Leu	Leu	Leu	Arg	Phe	Met	Leu	Gly	Ile	Pro	Leu
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Leu	Trp	Pro	Cys	Leu	Gly	Ala	Thr	Glu	Asn	Ser	Gln	Thr	Lys	Lys
				20					25					30
Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp
				35					40					45
Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser
				50					55					60

His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn		65	70	75
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe		80	85	90
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu		95	100	105
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile		110	115	120
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val		125	130	135
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp		140	145	150
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr		155	160	165
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser		170	175	180
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro		185	190	195
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser		200	205	210
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln		215	220	225
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr		230	235	240
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile		245	250	255
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro		260	265	270
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile		275	280	285
Gly	Glu	Asn	Ala	Glu	Met	Asp	Tyr	Ser	Ile	Glu	Glu	Asp	Asp	Ser		290	295	300
Gln	Thr	Phe	Asp	Ile	Ile	Thr	Asn	His	Glu	Thr	Gln	Glu	Gly	Ile		305	310	315
Val	Ile	Leu	Lys	Lys	Lys	Val	Asp	Phe	Glu	His	Gln	Asn	His	Tyr		320	325	330
Gly	Ile	Arg	Ala	Lys	Val	Lys	Asn	His	His	Val	Pro	Glu	Gln	Leu		335	340	345
Met	Lys	Tyr	His	Thr	Glu	Ala	Ser	Thr	Thr	Phe	Ile	Lys	Ile	Gln				

350	355	360
Val Glu Asp Val Asp Glu Pro Pro Leu Phe Leu Leu Pro Tyr Tyr		
365	370	375
Val Phe Glu Val Phe Glu Glu Thr Pro Gln Gly Ser Phe Val Gly		
380	385	390
Val Val Ser Ala Thr Asp Pro Asp Asn Arg Lys Ser Pro Ile Arg		
395	400	405
Tyr Ser Ile Thr Arg Ser Lys Val Phe Asn Ile Asn Asp Asn Gly		
410	415	420
Thr Ile Thr Thr Ser Asn Ser Leu Asp Arg Glu Ile Ser Ala Trp		
425	430	435
Tyr Asn Leu Ser Ile Thr Ala Thr Glu Lys Tyr Asn Ile Glu Gln		
440	445	450
Ile Ser Ser Ile Pro Leu Tyr Val Gln Val Leu Asn Ile Asn Asp		
455	460	465
His Ala Pro Glu Phe Ser Gln Tyr Tyr Glu Thr Tyr Val Cys Glu		
470	475	480
Asn Ala Gly Ser Gly Gln Val Ile Gln Thr Ile Ser Ala Val Asp		
485	490	495
Arg Asp Glu Ser Ile Glu Glu His His Phe Tyr Phe Asn Leu Ser		
500	505	510
Val Glu Asp Thr Asn Asn Ser Ser Phe Thr Ile Ile Asp Asn Gln		
515	520	525
Asp Asn Thr Ala Val Ile Leu Thr Asn Arg Thr Gly Phe Asn Leu		
530	535	540
Gln Glu Glu Pro Val Phe Tyr Ile Ser Ile Leu Ile Ala Asp Asn		
545	550	555
Gly Ile Pro Ser Leu Thr Ser Thr Asn Thr Leu Thr Ile His Val		
560	565	570
Cys Asp Cys Gly Asp Ser Gly Ser Thr Gln Thr Cys Gln Tyr Gln		
575	580	585
Glu Leu Val Leu Ser Met Gly Phe Lys Thr Glu Val Ile Ile Ala		
590	595	600
Ile Leu Ile Cys Ile Met Ile Ile Phe Gly Phe Ile Phe Leu Thr		
605	610	615
Leu Gly Leu Lys Gln Arg Arg Lys Gln Ile Leu Phe Pro Glu Lys		
620	625	630
Ser Glu Asp Phe Arg Glu Asn Ile Phe Gln Tyr Asp Asp Glu Gly		
635	640	645

Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg	650	655	660
Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser	665	670	675
Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro	680	685	690
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu	695	700	705
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr	710	715	720
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser	725	730	735
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu	740	745	750
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly	755	760	765
Ser	Ala	Val	Gln	Ser	Asn	Asn									770		

<210> 265
 <211> 349
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 24, 60, 141, 226, 228, 249, 252
 <223> unknown base

<400> 265
 atttcaaggc cagccatatt tttntgttga accaacaaca ggagtcataa 50
 gaatatatttn taaaatggat agagaactgc aagatgagta ttgggtaatc 100
 attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150
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 aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250
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<223> Synthetic oligonucleotide probe

<400> 266

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<212> DNA

<213> Artificial Sequence

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<400> 267

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<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

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gccacctgc aaactctccg ctttctgcac ctgccacccc tgagccagcg 200

cgggcccccg agcgagtcac ggccaacgcg gggctgcagc tgttgggctt 250

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gccatgtaag aggggctgtg gatgtcctgc gtgtcgcaga gcaccgggca 400

gatccagtgc aaagtctttg actccttgct gaatctgagc agcacattgc 450

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<211> 211
<212> PRT
<213> Homo sapiens

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Arg Ile Tyr Ser Tyr Ala Gly Asp Asn Ile Val Thr Ala Gln Ala
          35          40          45
Met Tyr Glu Gly Leu Trp Met Ser Cys Val Ser Gln Ser Thr Gly
          50          55          60
Gln Ile Gln Cys Lys Val Phe Asp Ser Leu Leu Asn Leu Ser Ser
          65          70          75
Thr Leu Gln Ala Thr Arg Ala Leu Met Val Val Gly Ile Leu Leu
          80          85          90
Gly Val Ile Ala Ile Phe Val Ala Thr Val Gly Met Lys Cys Met
          95          100          105
Lys Cys Leu Glu Asp Asp Glu Val Gln Lys Met Arg Met Ala Val
          110          115          120

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Ile Gly Gly Ala	Ile Phe Leu Leu Ala	Gly Leu Ala Ile Leu Val
125		130 135
Ala Thr Ala Trp Tyr Gly Asn Arg Ile	Val Gln Glu Phe Tyr Asp	
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Pro Met Thr Pro Val Asn Ala Arg Tyr	Glu Phe Gly Gln Ala Leu	
155	160	165
Phe Thr Gly Trp Ala Ala Ala Ser Leu	Cys Leu Leu Gly Gly Ala	
170	175	180
Leu Leu Cys Cys Ser Cys Pro Arg Lys	Thr Thr Ser Tyr Pro Thr	
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Val

<210> 271
 <211> 564
 <212> DNA
 <213> Homo sapiens

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 <222> 21, 69, 163, 434, 436, 444
 <223> unknown base

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 gctgttctctg tccc 564

<210> 272
 <211> 498

<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341
<223> unknown base

<400> 272
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tgaagtgtt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400
gggggcgcga tatttcttct tgcaggctctg gctatttttag ttgccacagc 450
atggtatggc aatagaatcg ttcaagaatt ctatgacct atgaccga 498

<210> 273
<211> 552
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394
<223> unknown base

<400> 273
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gctggcgaca acatcntgac cccagccat gtacgagggg ctttgaacgt 150
cngcgtgtcg caganacccg ggcagatcca gtgcaaagtc tttgactcct 200
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cattgggggc gcgatatttc ttcttgcagg tctggctatt tnnngttgcc 400
acagcatggt atggcaatag aatcgttcaa gaattctatg accctatgac 450

cccagtc aat gccaggtacg aatttgggtca ggctctcttc actggctggg 500
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ga 552

<210> 274

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407

<223> unknown base

<400> 274

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gtgcctact ttgctgttcc tgtccc 526

<210> 275

<211> 398

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274

<223> unknown base

<400> 275

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<210> 276
 <211> 495
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476
 <223> unknown base

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<210> 277
 <211> 200
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 34, 87, 138, 147, 163, 165-166, 172
 <223> unknown base

<400> 277
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<210> 278
<211> 542
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396
<223> unknown base

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<210> 279
<211> 548
<212> DNA
<213> Homo sapiens

<220>
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<222> 90, 115, 147, 228, 387
<223> unknown base

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<210> 280

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 280

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<210> 281

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 281

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<210> 282

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 282

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<210> 283

<211> 2285

<212> DNA

<213> Homo sapiens

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taaagcgggc gcagcattaa cgcttcccgc cccggtgacc tctcaggggt 200

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<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

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Lys	Leu	Gly	Asn	Pro	Thr	Asp	Arg	Asn	Val	Cys	Phe	Lys	Val	Lys
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Thr	Thr	Ala	Pro	Arg	Arg	Tyr	Cys	Val	Arg	Pro	Asn	Ser	Gly	Ile
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Phe	Asp	Tyr	Asp	Pro	Asn	Glu	Lys	Ser	Lys	His	Lys	Phe	Met	Val
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Gln	Ser	Met	Phe	Ala	Pro	Thr	Asp	Thr	Ser	Asp	Met	Glu	Ala	Val
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Trp	Lys	Glu	Ala	Lys	Pro	Glu	Asp	Leu	Met	Asp	Ser	Lys	Leu	Arg
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Glu	Ile	Asn	Lys	Ile	Ile	Ser	Thr	Thr	Ala	Ser	Lys	Thr	Glu	Thr
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Pro	Ile	Val	Ser	Lys	Ser	Leu	Ser	Ser	Ser	Leu	Asp	Asp	Thr	Glu
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Val	Lys	Lys	Val	Met	Glu	Glu	Cys	Lys	Arg	Leu	Gln	Gly	Glu	Val
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Gln	Arg	Leu	Arg	Glu	Glu	Asn	Lys	Gln	Phe	Lys	Glu	Glu	Asp	Gly
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Leu	Arg	Met	Arg	Lys	Thr	Val	Gln	Ser	Asn	Ser	Pro	Ile	Ser	Ala
				200					205					210
Leu	Ala	Pro	Thr	Gly	Lys	Glu	Glu	Gly	Leu	Ser	Thr	Arg	Leu	Leu
				215					220					225
Ala	Leu	Val	Val	Leu	Phe	Phe	Ile	Val	Gly	Val	Ile	Ile	Gly	Lys
				230					235					240

Ile Ala Leu

<210> 285
 <211> 418
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> unsure
 <222> 40, 53, 68, 119, 134, 177-178, 255
 <223> unknown base

<400> 285
 gtcagtcttc tagattgtcc ttatcccacc tttcaaccan tactcacatt 50
 tcnagcgccc aggtccangt ctgagcctga cttccccttg gggacctagc 100
 ctggagtcag gacaatggnt cgggctgcag aggnntagaa gcgagggcac 150
 cagcagtttt ggggtggggag caagggnga gagaaactct tcagcgaatc 200
 cttctagtag tagttgagag ttgactgtg aattaatttt atgccataaa 250
 agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300
 taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350
 ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400
 gttaacttta aaatgagc 418

<210> 286
 <211> 543
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 73, 97

<223> unknown base

<400> 286

tattgtaaag gccatttttaa accattggta ggccttggtg catgatgctg 50
gattacctcc ttaaatgaca ccnttcctcg cctggttggtg ctggccnttg 100
gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150
gtccccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250
aagggaattgc cactgtggca gcatcagacg tactcgtcat aagtgagagg 300
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcctt 350
gttcacttaa agggaccaag cttaaattgta ttggttcag tagtgaagtc 400
aaactgittat tcagagatgt ttaatgcata tttacttat ttaatgtatt 450
tcattctcatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500
gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287

<211> 270

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242

<223> unknown base

<400> 287

ccctggtggt tttgttcttt aattcgttgg tgtaattntt gggaagattg 50
cttgtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100
catatccatg ggattttaaat ttatcataac catgtgtaaa aagaaattaa 150
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250
agttaaaaat gtatagtaac 270

<210> 288

<211> 428

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 35, 116, 129, 197, 278, 294, 297, 349, 351

<223> unknown base

<400> 288
 ggtggcccat tcccggccca ggctgctttc cggtnnccag ttctgtccaa 50
 gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100
 gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150
 actgattgac ccagcgcttt ggaaataaat ggcagtgcct tgttcantta 200
 aaggggaccaa gctaaatttg tattgggttca tgtagtgaag tcaaactgtt 250
 attcagagat gtttaatgca tatttaantt atttaatgta tttnatntca 300
 tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350
 ntgttgggtg aactgggtatt gctgctggag ggctgtgggc tcctctgtct 400
 ttggagagtc tggatcatgtg gaggtggg 428

<210> 289
 <211> 320
 <212> DNA
 <213> Homo sapiens

<400> 289
 tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50
 atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100
 tactcgatcat aagtgaagagg cgtgtgttga ctgattgacc cagcgctttg 150
 gaaataaatg gcagtgcctt gttcacttaa agggaccaag ctaaatttgt 200
 attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250
 atttaactta tttaatgtat ttcattctcat gttttcttat tgtcacaaga 300
 gtacagttaa tgctgcgtgc 320

<210> 290
 <211> 609
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,
 447, 481, 513, 532, 584, 598
 <223> unknown base

<400> 290
 aaacctttta aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50
 gaaaccntgn gtaatgccac aatggcatat tgtaaattgc attttaaaca 100
 ttggtaggcc ttggtacatg atgctggatt acctctctta aatgacacc 150
 cttcctcgcc tgttgggtgt ggcccttggg gagctngagc ccagcatgct 200

ggggagtgcg gtctgtcca cacagtagtc cccangtggc ccantcccgg 250
 cccaggctgc tttccgtgtc ttcagttctg tccaagccat cagctccttg 300
 ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350
 cagangtant ngtcataagt gagagggcgtg tggttgantga ttgaccagc 400
 gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450
 atttgtattg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500
 atgcatatth aanttattta atgtatttca tntcatgttt tcttattgtc 550
 acaagggtag agttaatgct gcgtgtgtgt gaantctgtt ggggtgaantg 600
 gtattgctg 609

<210> 291
 <211> 493
 <212> DNA
 <213> Homo sapiens

<400> 291
 ggcccttggg gagctggagc ccagcatgct ggggagtgcg gtcagctcca 50
 cacagtagtc cccacgtggc ccactcccgg cccaggctgc tttccgtgtc 100
 ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150
 aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200
 gagagggcgtg tggttgactga ttgaccagc gctttggaaa taaatggcag 250
 tgctttgttc acttaaaggg accaagctaa atttgtattg gttcatgtag 300
 tgaagtcaaa ctgttattca gagatgttta atgcatatth aacttattta 350
 atgtatttca tctcatgttt tcttattgtc acaagagtag agttaatgct 400
 gcgtgtgtgt gaactctgtt ggggtgaactg gtattgctgc tggagggctg 450
 tgggctcctc tgtctctgga gagtctggtc atgtggaggt ggg 493

<210> 292
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 292
 gcaccaccgt aggtacttgt gtgaggc 27

<210> 293
 <211> 23
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaaagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

gcgagctccg ggtgctgtgg cccggccttg gcggggcggc ctccggctca 50

ggctggctga gaggtccca gctgcagcgt ccccgccgc ctctcgga 100

gctctgatct cagctgacag tgcctcggg gaccaaaca gcctggcagg 150

gtctcacttt gttgccagg ctggagttca gtgccatgat catggtttac 200

tgcagccttg acctcctggg ttcaagcgt cctgctgagt agctgggact 250

acaggacaaa attagaagat caaatggaa aatatgctgc tttggttgat 300

atctttcacc cctgggtgga cctcattga tggatctgaa atggaatggg 350

atcttatgtg gcaattgaga aaggtacccc ggattgtcag tgaaaggact 400

ttccatctca ccagccccgc atttgaggca gatgctaaga tgatggtaaa 450

tacagtgtgt ggcacgaat gccagaaaga actcccaact cccagccttt 500

ctgaattgga ggattatctt tcctatgaga ctgtctttga gaatggcacc 550

cgaaccttaa ccagggtgaa agttcaagat ttggttcttg agccgactca 600

aaatatcacc acaaaggag tatctgttag gagaaagaga caggtgtatg 650

gcaccgacag caggttcagc atcttgga aaaggttctt aaccaatttc 700

cctttcagca cagctgtgaa gctttccacg ggctgtagtg gcattctcat 750

ttcccctcag catgttctaa ctgctgccca ctgtgttcat gatggaaagg 800

actatgtcaa agggagtaaa aagctaagg taggggttgtt gaagatgagg 850

cttcacaaat tatgaatgat catgtgttga aagccacatt attttatgct 2350
 atacattcta tgtatgaggt gctacatttt taggacaaag aattctgtaa 2400
 tctttttcaa gaaagagtct ttttctcctt gacaaaatcc agcttttgta 2450
 tgaggactat aggggtgaatt ctctgattag taattttaga tatgtccttt 2500
 cctaaaaatg aataaaattt atgaatatga 2530

<210> 296

<211> 413

<212> PRT

<213> Homo sapiens

<400> 296

Met	Glu	Asn	Met	Leu	Leu	Trp	Leu	Ile	Phe	Phe	Thr	Pro	Gly	Trp	1	5	10	15
Thr	Leu	Ile	Asp	Gly	Ser	Glu	Met	Glu	Trp	Asp	Phe	Met	Trp	His	20	25	30	
Leu	Arg	Lys	Val	Pro	Arg	Ile	Val	Ser	Glu	Arg	Thr	Phe	His	Leu	35	40	45	
Thr	Ser	Pro	Ala	Phe	Glu	Ala	Asp	Ala	Lys	Met	Met	Val	Asn	Thr	50	55	60	
Val	Cys	Gly	Ile	Glu	Cys	Gln	Lys	Glu	Leu	Pro	Thr	Pro	Ser	Leu	65	70	75	
Ser	Glu	Leu	Glu	Asp	Tyr	Leu	Ser	Tyr	Glu	Thr	Val	Phe	Glu	Asn	80	85	90	
Gly	Thr	Arg	Thr	Leu	Thr	Arg	Val	Lys	Val	Gln	Asp	Leu	Val	Leu	95	100	105	
Glu	Pro	Thr	Gln	Asn	Ile	Thr	Thr	Lys	Gly	Val	Ser	Val	Arg	Arg	110	115	120	
Lys	Arg	Gln	Val	Tyr	Gly	Thr	Asp	Ser	Arg	Phe	Ser	Ile	Leu	Asp	125	130	135	
Lys	Arg	Phe	Leu	Thr	Asn	Phe	Pro	Phe	Ser	Thr	Ala	Val	Lys	Leu	140	145	150	
Ser	Thr	Gly	Cys	Ser	Gly	Ile	Leu	Ile	Ser	Pro	Gln	His	Val	Leu	155	160	165	
Thr	Ala	Ala	His	Cys	Val	His	Asp	Gly	Lys	Asp	Tyr	Val	Lys	Gly	170	175	180	
Ser	Lys	Lys	Leu	Arg	Val	Gly	Leu	Leu	Lys	Met	Arg	Asn	Lys	Ser	185	190	195	
Gly	Gly	Lys	Lys	Arg	Arg	Gly	Ser	Lys	Arg	Ser	Arg	Arg	Glu	Ala	200	205	210	

<220>
<223> Synthetic oligonucleotide probe

<400> 298
catcgttccc gtgaatccag aggc 24

<210> 299
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 299
gaagggaggc cttcctttca gtggacccgg gtcaagaata cccac 45

<210> 300
<211> 1869
<212> DNA
<213> Homo sapiens

<400> 300
aatgtgagag gggctgatgg aagctgatag gcaggactgg agtgtttagca 50
ccagtactgg atgtgacagc aggcagagga gcacttagca gcttattcag 100
tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150
gcaactcctg gcacactgct cctctttctg gctttcctgc tcctgagttc 200
caggaccgca cgtcccgagg aggaccggga cggcctatgg gatgcctggg 250
gcccatggag tgaatgctca cgcacctgcg ggggaggggc ctccactct 300
ctgaggcgct gcctgagcag caagagctgt gaaggaagaa atatccgata 350
cagaacatgc agtaatgtgg actgcccacc agaagcaggt gatttccgag 400
ctcagcaatg ctcagctcat aatgatgtca agcaccatgg ccagttttat 450
gaatggcttc ctgtgtctaa tgaccctgac aacctatggt cactcaagtg 500
ccaagccaaa ggaacaaccc tggttgttga actagcacct aaggtcttag 550
atggtacgcg ttgctataca gaatctttgg atatgtgcat cagtggttta 600
tgccaaattg ttggctgca tcaccagctg ggaagcacg tcaaggaaga 650
taactgtggg gtctgcaacg gagatgggtc cacctgccgg ctggtccgag 700
ggcagtataa atcccagctc tccgcaacca aatcgatga tactgtgggt 750
gcacttcctt atggaagtag acatattcgc cttgtcttaa aaggtcctga 800
tcacttatat ctggaaacca aaaccctcca ggggactaaa ggtgaaaaca 850
gtctcagctc cacaggaact ttccttggtg acaattctag tgtggacttc 900

Leu	Ser	Ser	Lys	Ser 65	Cys	Glu	Gly	Arg	Asn 70	Ile	Arg	Tyr	Arg	Thr 75
Cys	Ser	Asn	Val	Asp 80	Cys	Pro	Pro	Glu	Ala 85	Gly	Asp	Phe	Arg	Ala 90
Gln	Gln	Cys	Ser	Ala 95	His	Asn	Asp	Val	Lys 100	His	His	Gly	Gln	Phe 105
Tyr	Glu	Trp	Leu	Pro 110	Val	Ser	Asn	Asp	Pro 115	Asp	Asn	Pro	Cys	Ser 120
Leu	Lys	Cys	Gln	Ala 125	Lys	Gly	Thr	Thr	Leu 130	Val	Val	Glu	Leu	Ala 135
Pro	Lys	Val	Leu	Asp 140	Gly	Thr	Arg	Cys	Tyr 145	Thr	Glu	Ser	Leu	Asp 150
Met	Cys	Ile	Ser	Gly 155	Leu	Cys	Gln	Ile	Val 160	Gly	Cys	Asp	His	Gln 165
Leu	Gly	Ser	Thr	Val 170	Lys	Glu	Asp	Asn	Cys 175	Gly	Val	Cys	Asn	Gly 180
Asp	Gly	Ser	Thr	Cys 185	Arg	Leu	Val	Arg	Gly 190	Gln	Tyr	Lys	Ser	Gln 195
Leu	Ser	Ala	Thr	Lys 200	Ser	Asp	Asp	Thr	Val 205	Val	Ala	Leu	Pro	Tyr 210
Gly	Ser	Arg	His	Ile 215	Arg	Leu	Val	Leu	Lys 220	Gly	Pro	Asp	His	Leu 225
Tyr	Leu	Glu	Thr	Lys 230	Thr	Leu	Gln	Gly	Thr 235	Lys	Gly	Glu	Asn	Ser 240
Leu	Ser	Ser	Thr	Gly 245	Thr	Phe	Leu	Val	Asp 250	Asn	Ser	Ser	Val	Asp 255
Phe	Gln	Lys	Phe	Pro 260	Asp	Lys	Glu	Ile	Leu 265	Arg	Met	Ala	Gly	Pro 270
Leu	Thr	Ala	Asp	Phe 275	Ile	Val	Lys	Ile	Arg 280	Asn	Ser	Gly	Ser	Ala 285
Asp	Ser	Thr	Val	Gln 290	Phe	Ile	Phe	Tyr	Gln 295	Pro	Ile	Ile	His	Arg 300
Trp	Arg	Glu	Thr	Asp 305	Phe	Phe	Pro	Cys	Ser 310	Ala	Thr	Cys	Gly	Gly 315
Gly	Tyr	Gln	Leu	Thr 320	Ser	Ala	Glu	Cys	Tyr 325	Asp	Leu	Arg	Ser	Asn 330
Arg	Val	Val	Ala	Asp 335	Gln	Tyr	Cys	His	Tyr 340	Tyr	Pro	Glu	Asn	Ile 345
Lys	Pro	Lys	Pro	Lys	Leu	Gln	Glu	Cys	Asn	Leu	Asp	Pro	Cys	Pro

Ala	Ser	Asp	Gly	Tyr	Lys	Gln	Ile	Met	Pro	Tyr	Asp	Leu	Tyr	His
				365					370					375
Pro	Leu	Pro	Arg	Trp	Glu	Ala	Thr	Pro	Trp	Thr	Ala	Cys	Ser	Ser
				380					385					390
Ser	Cys	Gly	Gly	Gly	Ile	Gln	Ser	Arg	Ala	Val	Ser	Cys	Val	Glu
				395					400					405
Glu	Asp	Ile	Gln	Gly	His	Val	Thr	Ser	Val	Glu	Glu	Trp	Lys	Cys
				410					415					420
Met	Tyr	Thr	Pro	Lys	Met	Pro	Ile	Ala	Gln	Pro	Cys	Asn	Ile	Phe
				425					430					435
Asp	Cys	Pro	Lys	Trp	Leu	Ala	Gln	Glu	Trp	Ser	Pro	Cys	Thr	Val
				440					445					450
Thr	Cys	Gly	Gln	Gly	Leu	Arg	Tyr	Arg	Val	Val	Leu	Cys	Ile	Asp
				455					460					465
His	Arg	Gly	Met	His	Thr	Gly	Gly	Cys	Ser	Pro	Lys	Thr	Lys	Pro
				470					475					480
His	Ile	Lys	Glu	Glu	Cys	Ile	Val	Pro	Thr	Pro	Cys	Tyr	Lys	Pro
				485					490					495
Lys	Glu	Lys	Leu	Pro	Val	Glu	Ala	Lys	Leu	Pro	Trp	Phe	Lys	Gln
				500					505					510
Ala	Gln	Glu	Leu	Glu	Glu	Gly	Ala	Ala	Val	Ser	Glu	Glu	Pro	Ser
				515					520					525

<210> 302
 <211> 1533
 <212> DNA
 <213> Homo sapiens

<400> 302
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 ctcgggcctg acagatggca gtggccactg cggcggcagt actggccgct 100
 ctgggcgggg cgctgtggct ggcggcccgc cggttcgtgg ggcccagggt 150
 ccagcggtcg cgcagaggcg gggaccccg cctcatgcac gggaagactg 200
 tgctgatcac cggggcgaa acgcggcctgg gccgcgccac ggccgcccag 250
 ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300
 cgccgaggag gcggcgggtc agctccgcgc cgagctccgc caggccgcgcg 350
 agtgcggccc agagcctggc gtcagcgggg tgggcgagct catagtccgg 400
 gagctggacc tcgcctcgct gcgctcggtg cgcgccttct gccaggaaat 450

gctccaggaa gagcctaggc tggatgtctt gatcaataac gcagggatct 500
tccagtgtcc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550
gtgaaccatc tggggcactt tctactcacc aatcttctcc ttggactcct 600
caaaagtcca gctcccagca ggattgtggt agtttcttcc aaactttata 650
aatacggaga catcaatttt gatgacttga acagtgaaca aagctataat 700
aaaagctttt gttatagccg gagcaaactg gctaacattc tttttaccag 750
ggaactagcc cgccgcttag aaggcacaaa tgtcaccgtc aatgtgttgc 800
atcctggtat tgtacggaca aatctgggga ggcacataca cattccactg 850
ttggtcaaac cactcttcaa tttggtgtca tgggcttttt tcaaaactcc 900
agtagaaggt gccagactt ccatttattt ggctcttca cctgaggtag 950
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cccaaagcta tggatgaatc tgttgcaaga aaactctggg atatcagtga 1050
agtgatggtt ggctgtctaa aataggaaca aggagtaaaa gagctgttta 1100
taaaactgca tatcagttat atctgtgatc aggaatggtg tggattgaga 1150
acttgttact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200
ggtacatgtg ggtattttgg agttactgaa aaattatttt tgggataaga 1250
gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300
aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350
tggatgacat attaataattt gtcagaatta agtgactcaa agtgctatcg 1400
agagggtttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450
ttactacaat gtttgggtgtt tgtgtggaaa ttatctgcct ggtgtgtgca 1500
cacaagtctt acttgaata aatttactgg tac 1533

<210> 303

<211> 336

<212> PRT

<213> Homo sapiens

<400> 303

Met	Ala	Val	Ala	Thr	Ala	Ala	Ala	Val	Leu	Ala	Ala	Leu	Gly	Gly
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Ala	Leu	Trp	Leu	Ala	Ala	Arg	Arg	Phe	Val	Gly	Pro	Arg	Val	Gln
			20					25					30	
Arg	Leu	Arg	Arg	Gly	Gly	Asp	Pro	Gly	Leu	Met	His	Gly	Lys	Thr
			35					40					45	

Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala	
				50					55					60	
Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg	
				65					70					75	
Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu	
				80					85					90	
Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly	
				95					100					105	
Val	Gly	Glu	Leu	Ile	Val	Arg	Glu	Leu	Asp	Leu	Ala	Ser	Leu	Arg	
				110					115					120	
Ser	Val	Arg	Ala	Phe	Cys	Gln	Glu	Met	Leu	Gln	Glu	Glu	Pro	Arg	
				125					130					135	
Leu	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Phe	Gln	Cys	Pro	Tyr	
				140					145					150	
Met	Lys	Thr	Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	
				155					160					165	
Leu	Gly	His	Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Gly	Leu	Leu	Lys	
				170					175					180	
Ser	Ser	Ala	Pro	Ser	Arg	Ile	Val	Val	Val	Ser	Ser	Lys	Leu	Tyr	
				185					190					195	
Lys	Tyr	Gly	Asp	Ile	Asn	Phe	Asp	Asp	Leu	Asn	Ser	Glu	Gln	Ser	
				200					205					210	
Tyr	Asn	Lys	Ser	Phe	Cys	Tyr	Ser	Arg	Ser	Lys	Leu	Ala	Asn	Ile	
				215					220					225	
Leu	Phe	Thr	Arg	Glu	Leu	Ala	Arg	Arg	Leu	Glu	Gly	Thr	Asn	Val	
				230					235					240	
Thr	Val	Asn	Val	Leu	His	Pro	Gly	Ile	Val	Arg	Thr	Asn	Leu	Gly	
				245					250					255	
Arg	His	Ile	His	Ile	Pro	Leu	Leu	Val	Lys	Pro	Leu	Phe	Asn	Leu	
				260					265					270	
Val	Ser	Trp	Ala	Phe	Phe	Lys	Thr	Pro	Val	Glu	Gly	Ala	Gln	Thr	
				275					280					285	
Ser	Ile	Tyr	Leu	Ala	Ser	Ser	Pro	Glu	Val	Glu	Gly	Val	Ser	Gly	
				290					295					300	
Arg	Tyr	Phe	Gly	Asp	Cys	Lys	Glu	Glu	Glu	Leu	Leu	Pro	Lys	Ala	
				305					310					315	
Met	Asp	Glu	Ser	Val	Ala	Arg	Lys	Leu	Trp	Asp	Ile	Ser	Glu	Val	
				320					325					330	
Met	Val	Gly	Leu	Leu	Lys										

<210> 304
 <211> 521
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 20, 34, 62, 87, 221, 229
 <223> unknown base

<400> 304
 ggggattgta aagaggaagn actgtgccca aagntatgga tgaatctgtt 50
 gcaagaaaat tntgggatat cagtgaagtg atggttngcc tgctaaaata 100
 ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150
 gtgatcagga atgggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200
 tttgatattg gaatagcctg ntaagaggna catgtgggta ttttgagatt 250
 actgaaaaat tatttttggg ataagagaat ttcagcaaag atgtttttaa 300
 tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350
 attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400
 gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450
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ccagcgcctg tccctgtcac ggacccagc gttaccatgc atcctgccgt 150
cttcctatcc ttacccgacc tcagatgctc cttctgtctc ctggtaactt 200
gggtttttac tctgttaaca actgaaataa caagtcttgc tacagagaat 250
atagatgaaa ttttaaacia tgctgatgtt gctttagtaa atttttatgc 300
tgactgggtgt cgtttcagtc agatgttgca tccaattttt gaggaagctt 350
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400
agagttgatt gtgatcagca ctctgacata gcccagagat acaggataag 450
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 500
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tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750
tggcgacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800
tgtacttggg agctatgaca aattttgatg tgacttacia ttggattcaa 850
gataaatgtg ttcctcttgt ccgagaaata acatttgaaa atggagagga 900
attgacagaa gaaggactgc cttttotcat actctttcac atgaaagaag 950
atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000
agtgaaaaag gtacaataaa cttttttacat gccgattgtg acaaatttag 1050

acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100
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Ile	Thr	Ser	Leu	Ala	Thr	Glu	Asn	Ile	Asp	Glu	Ile	Leu	Asn	Asn	35	40	45	
Ala	Asp	Val	Ala	Leu	Val	Asn	Phe	Tyr	Ala	Asp	Trp	Cys	Arg	Phe	50	55	60	
Ser	Gln	Met	Leu	His	Pro	Ile	Phe	Glu	Glu	Ala	Ser	Asp	Val	Ile	65	70	75	
Lys	Glu	Glu	Phe	Pro	Asn	Glu	Asn	Gln	Val	Val	Phe	Ala	Arg	Val	80	85	90	
Asp	Cys	Asp	Gln	His	Ser	Asp	Ile	Ala	Gln	Arg	Tyr	Arg	Ile	Ser	95	100	105	
Lys	Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Arg	Asn	Gly	Met	Met	Met	Lys	110	115	120	
Arg	Glu	Tyr	Arg	Gly	Gln	Arg	Ser	Val	Lys	Ala	Leu	Ala	Asp	Tyr	125	130	135	
Ile	Arg	Gln	Gln	Lys	Ser	Asp	Pro	Ile	Gln	Glu	Ile	Arg	Asp	Leu	140	145	150	
Ala	Glu	Ile	Thr	Thr	Leu	Asp	Arg	Ser	Lys	Arg	Asn	Ile	Ile	Gly	155	160	165	

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Tyr	Phe	Glu	Gln	Lys	Asp	Ser	Asp	Asn	Tyr	Arg	Val	Phe	Glu	Arg	
				170					175					180	
Val	Ala	Asn	Ile	Leu	His	Asp	Asp	Cys	Ala	Phe	Leu	Ser	Ala	Phe	
				185					190					195	
Gly	Asp	Val	Ser	Lys	Pro	Glu	Arg	Tyr	Ser	Gly	Asp	Asn	Ile	Ile	
				200					205					210	
Tyr	Lys	Pro	Pro	Gly	His	Ser	Ala	Pro	Asp	Met	Val	Tyr	Leu	Gly	
				215					220					225	
Ala	Met	Thr	Asn	Phe	Asp	Val	Thr	Tyr	Asn	Trp	Ile	Gln	Asp	Lys	
				230					235					240	
Cys	Val	Pro	Leu	Val	Arg	Glu	Ile	Thr	Phe	Glu	Asn	Gly	Glu	Glu	
				245					250					255	
Leu	Thr	Glu	Glu	Gly	Leu	Pro	Phe	Leu	Ile	Leu	Phe	His	Met	Lys	
				260					265					270	
Glu	Asp	Thr	Glu	Ser	Leu	Glu	Ile	Phe	Gln	Asn	Glu	Val	Ala	Arg	
				275					280					285	
Gln	Leu	Ile	Ser	Glu	Lys	Gly	Thr	Ile	Asn	Phe	Leu	His	Ala	Asp	
				290					295					300	
Cys	Asp	Lys	Phe	Arg	His	Pro	Leu	Leu	His	Ile	Gln	Lys	Thr	Pro	
				305					310					315	
Ala	Asp	Cys	Pro	Val	Ile	Ala	Ile	Asp	Ser	Phe	Arg	His	Met	Tyr	
				320					325					330	
Val	Phe	Gly	Asp	Phe	Lys	Asp	Val	Leu	Ile	Pro	Gly	Lys	Leu	Lys	
				335					340					345	
Gln	Phe	Val	Phe	Asp	Leu	His	Ser	Gly	Lys	Leu	His	Arg	Glu	Phe	
				350					355					360	
His	His	Gly	Pro	Asp	Pro	Thr	Asp	Thr	Ala	Pro	Gly	Glu	Gln	Ala	
				365					370					375	
Gln	Asp	Val	Ala	Ser	Ser	Pro	Pro	Glu	Ser	Ser	Phe	Gln	Lys	Leu	
				380					385					390	
Ala	Pro	Ser	Glu	Tyr	Arg	Tyr	Thr	Leu	Leu	Arg	Asp	Arg	Asp	Glu	
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Leu

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- <211> 182
- <212> DNA
- <213> Homo sapiens
- <220>
- <221> unsure

<222> 36, 48
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 ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100
 caaccctcaa attgttttcgt aatgggatga tgatgaagag agaatacagg 150
 ggtcagcgat cagtgaagc attggcagat ta 182

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 <222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396
 <223> unknown base

<400> 311
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 cggagcccag ccctttccta acccaacca acctagccn gtcccagccg 150
 ccagcgctg tccctgtcnc gganccagc gtnaccatgc atcctgccgt 200
 cttcctatcc ttaccgacc tcagatgctc cttctgctc ctggtaactt 250
 gggtttttac tcctgtaaca actgaaataa cnngtcttga tacnnagaat 300
 atagatgaaa ttttaaacna tgctgatgtg gctttagtca atttttatgc 350
 tgactgggtg cgtttcagtc agatgtggca tccaattttt gaggangctt 400
 ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450
 agagttgatt gtgatcagca ctctgacata gcccagagat acaggataag 500
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 aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

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 tgagaggcct ctctggaagt tg 22

<210> 313
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gtcagcgatc agtgaaagc 19

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ccagaatgaa gtagctcggc 20

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ccgactcaaa atgcattgtc 20

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catttggcag gaattgtcc 19

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<400> 317
ggtgctatag gccaaagg 18

<210> 318
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<223> Synthetic oligonucleotide probe

<400> 318

ctgtatctct gggctatgtc agag 24

<210> 319

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<212> DNA

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<400> 319

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<210> 320

<211> 46

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 320

cgtcttcccta tccttaccgc acctcagatg ctcccttctg ctccctg 46

<210> 321

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<212> DNA

<213> Homo sapiens

<400> 321

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gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150

taccctgaat ccccttgtag tcccagagta cctcatccac gctttcttct 200

gtgtcatgtt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250

cccctcttgg catatcatat ttggaggtat atgagtagac cagtgatgag 300

tggcccagga ctctatgacc ctacaacccat catgaatgca gatattctag 350

catattgtca gaaggaagga tgggtgcaa tagcttttta tcttctagca 400

tttttttact acctatatgg catgatctat gttttggtga gctcttagaa 450

caacacacag aagaattggc ccagttaagt gcatgcaaaa agccacccaaa 500

tgaagggtt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550

tgatcagtta ctttaaaaaa tgactcctta ttttttaa at gtttccacat 600
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 cttgtagggc tcatttttgg ttcattgaaa cagtatctaa ttataaatta 850
 gctgtagata tcagggtgctt ctgatgaagt gaaaatgtat atctgactag 900
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 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050
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<210> 322

<211> 144

<212> PRT

<213> Homo sapiens

<400> 322

Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu
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Leu Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala
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Phe Asp Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys
 35 40 45

Asn Thr Leu Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala
 50 55 60

Phe Phe Cys Val Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu
 65 70 75

Gly Leu Asn Met Pro Leu Leu Ala Tyr His Ile Trp Arg Tyr Met
 80 85 90

Ser Arg Pro Val Met Ser Gly Pro Gly Leu Tyr Asp Pro Thr Thr
 95 100 105

Ile	Met	Asn	Ala	Asp	Ile	Leu	Ala	Tyr	Cys	Gln	Lys	Glu	Gly	Trp
				110					115					120
Cys	Lys	Leu	Ala	Phe	Tyr	Leu	Leu	Ala	Phe	Phe	Tyr	Tyr	Leu	Tyr
				125					130					135
Gly	Met	Ile	Tyr	Val	Leu	Val	Ser	Ser						
				140										

<210> 323
 <211> 477
 <212> DNA
 <213> Homo sapiens

<400> 323
 attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50
 tgtaataccc tgaatcccct tgtactcca gactaccta tccacgcttt 100
 cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150
 atatgcccct cttggcatat catatttgga ggtatatgag tagaccagtg 200
 atgagtggcc caggactcta tgaccctaca accatcatga atgcagatat 250
 tctagcatat tgtcagaagg aaggatgggtg caaattagct ttttatcttc 300
 tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350
 tagaacaaca cacagaagaa ttggtccagt taagtgcattg caaaaagcca 400
 ccaaataaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450
 gaatctgatc agttacttta aaaaatg 477

<210> 324
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 324
 tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 325
 caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 326
gtgcagcaga gtggcttaca 20

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 327
actggaccaa ttcttctgtg 20

<210> 328
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 328
gatattctag catattgtca gaaggaagga tggcgcaaat tagct 45

<210> 329
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 329
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50
tgtgacagag gggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100
ggacccaact ggggctcccg ccgctgctgc tgctgaccat ggccttggcc 150
ggaggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250
accotaagga agaggagttg tacgcatgtc agagaggttg caggctgttt 300
tcaatttgtc agtttgtgga tgatggaatt gacttaaadc gaactaaatt 350
ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450
caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttcctct 500

aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300

tttcctctaa ctctggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332

<211> 562

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 47

<223> unknown base

<400> 332

cacactggcc ggatctttta gattcctttg accttgacca agggtcngga 50

aaacagcaac aagctgagct gctgtgacag agggaacaag atggcggcgc 100

cgaagggagc ctttgggtga ggacccaact ggggctcccg ccgctgctgc 150

tgctgaccat ggccttggcc ggaggttcgg ggaccgcttc ggctgaagca 200

tttgactcgg tcttgggtga tacggcgtct tgccaccggg cctgtcagtt 250

gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300

agagagggtg caggctgttt tcaatttgtc agtttgtgga tgatggaatt 350

gacttaaadc gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400

ttcccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450

tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500

atgcacctac tctttcctct aactctggtg aggtcattct ggagtgcacat 550

gatggactcc gc 562

<210> 333

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 333

acaagctgag ctgctgtgac ag 22

<210> 334

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 334
tgattctggc aaccaagatg gc 22

<210> 335

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 335

atggccttgg ccggaggttc ggggaccgct tcggctgaag 40

<210> 336

<211> 1885

<212> DNA

<213> Homo sapiens

<400> 336

gcgaggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50
cgccccggag gtggggcgcc gctggggccg gcccgcacgg gcttcatctg 100
agggcgacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150
gcgacaagct gccggagctg caatgggccg cggctgggga ttcttgtttg 200
gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250
cccccgaga cagcggcaca gaggtgcttc tgccagggtta gtggttactt 300
ggatgattgt acctgtgatg ttgaaaccat tgatagattt aataactaca 350
ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400
tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600
tctgagttag gaaacacaga aggctgttct tcagtggacc aagcatgatg 650
attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700
gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800
agccacagac aattaaaaga cctttaaatc ctttggcttc tggtaaggg 850
acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900
aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950

tgcatttgag tgcaagatat cttttacaag agacctggtt agaaaagaaa 1000
 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050
 tgaaggagaa ggtccaagaa ggcttaagaa cttgtatttt ctctacttaa 1100
 tagaactaag ggcttttatcc aaagtgttac cattcttcga gcgcccagat 1150
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatggt 1200
 acttctggaa atacttcatt aaatcaagtc atttcctttg cattttgatg 1250
 agaattcatt ttttgctggg gataaaaaag aagcacacaa actaaaggag 1300
 gactttcgac tgcattttag aaatatttca agaattatgg attgtgttgg 1350
 ttgtttttaa tgtcgtctgt ggggaaagct tcagactcag ggtttgggca 1400
 ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450
 agtggaccta gttatgaatt ccatctaacc agacaagaaa tagtatcatt 1500
 attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaact 1550
 tcaggaactt gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600
 ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650
 atagcaatga cagtcttaag ccaaacattt tatataaagt tgcttttgta 1700
 aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750
 gtctatgtat aatactactg tgagtaaaag taatacttta ataatgtggg 1800
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaaaa 1850
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1885

<210> 337

<211> 468

<212> PRT

<213> Homo sapiens

<400> 337

Met	Gly	Arg	Gly	Trp	Gly	Phe	Leu	Phe	Gly	Leu	Leu	Gly	Ala	Val
1				5					10					15
Trp	Leu	Leu	Ser	Ser	Gly	His	Gly	Glu	Glu	Gln	Pro	Pro	Glu	Thr
			20					25						30
Ala	Ala	Gln	Arg	Cys	Phe	Cys	Gln	Val	Ser	Gly	Tyr	Leu	Asp	Asp
			35						40					45
Cys	Thr	Cys	Asp	Val	Glu	Thr	Ile	Asp	Arg	Phe	Asn	Asn	Tyr	Arg
			50						55					60
Leu	Phe	Pro	Arg	Leu	Gln	Lys	Leu	Leu	Glu	Ser	Asp	Tyr	Phe	Arg
			65						70					75

365	370	375
Glu Asp Phe Arg Leu His Phe Arg Asn Ile Ser Arg Ile Met Asp		
380	385	390
Cys Val Gly Cys Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln Thr		
395	400	405
Gln Gly Leu Gly Thr Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu		
410	415	420
Ile Ala Asn Met Pro Glu Ser Gly Pro Ser Tyr Glu Phe His Leu		
425	430	435
Thr Arg Gln Glu Ile Val Ser Leu Phe Asn Ala Phe Gly Arg Ile		
440	445	450
Ser Thr Ser Val Lys Glu Leu Glu Asn Phe Arg Asn Leu Leu Gln		
455	460	465

Asn Ile His

<210> 338
 <211> 507
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 101, 263, 376, 397, 426
 <223> unknown base

<400> 338
 gctggaaata tggatgtcat ctacgagaaa ctgttttaag ccacagacaa 50
 ttaaaagacc tttaaatoct ttggcttctg gtcaagggac aagtgaagag 100
 nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150
 ctacagactt atatctggcc tacatgcaag cattaatgtg ctttgagtg 200
 caagatatct tttaacaagag acctgggttag aaaagaaatg gggacacaac 250
 attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300
 tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350
 ctttatccaa agtggtacca ttcttngagc gccagattt tcaactnttt 400
 actggaaata aaattcagga tgaggnaaac aaaatgttac ttttgaaat 450
 acttcatgaa atcaagtcac ttcccttgca ttttgatgag aattcatttt 500
 tttgctg 507

<210> 339
 <211> 20

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 339
 aagctgccgg agctgcaatg 20

 <210> 340
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 340
 ttgctttctta atcctgagcg c 21

 <210> 341
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 341
 aaaggaggac tttcgactgc 20

 <210> 342
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 342
 agagattcat ccaactgctcc aagtcg 26

 <210> 343
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 343
 tgtccagaaa caggcacata tcagc 25

 <210> 344
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 344
agacagcggc acagaggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345
<211> 1486
<212> DNA
<213> Homo sapiens

<400> 345
cggacgcgtg ggcggacgcg tgggcggacg cgtgggttgg gagggggcag 50
gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100
ggactttctca tactggacag aaaccgatca ggcatggaac tccccttcgt 150
cactcacctg ttcttgcccc tgggtgttct gacaggtctc tgctccccct 200
ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250
gaatttggat acagtgtctt acaacatgtt gggggtggac agcgatggat 300
gctgggtgggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350
tttatcgctg ccctgtaggg gggggccaca atgccccatg tgccaagggc 400
cacttaggtg actaccaact gggaaattca tctcatcctg ctgtgaatat 450
gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500
tgagctaagg agaggggtggg ggcagtgtct ctgaagggtcc ataaaagaaa 550
aaagagaagt gtggttaaggg aaaatgggtct gtgtggaggg gtcaaggagt 600
taaaaaccct agaaagcaaa aggtaggtta tgtcaggag tagtcttcat 650
gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700
gtaactatct ccccatccc caggcctgtg cccctctctg gtctcgtgct 750
tgtggcagct ctgtcttcag ttctgggata tgtgccctg tggatgcttc 800
attccagcct cagggaagcc tggcaccac tgccaacgt gagccagagg 850
aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900
gggcaaagcg gtatgatgcc tggcaaaggg cctgcatggc tatcctcatt 950
gctacctaat gtgcttgcaa aagctccatg tttcctaaca gattcagact 1000
cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggc 1050
caaggtgggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100
catggtgaaa ctccatctct actaaaaaaaa aaaaaatata aaaattagct 1150

ggggtgcgcta gtgcatgcct gtaatctcat ctactcggga ggctaagaca 1200
 ggagactctc acttcaaccc aggaggtgga ggttgcggtg agccaagatt 1250
 gtgcctctgc actctagcgt gggtgacaga gtaagcgaga ctccatctca 1300
 aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350
 gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400
 gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450
 agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 346
 Met Glu Leu Pro Phe Val Thr His Leu Phe Leu Pro Leu Val Phe
 1 5 10 15
 Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp Glu His His Pro
 20 25 30
 Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val
 35 40 45
 Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala
 50 55 60
 Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr Arg
 65 70 75
 Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His
 80 85 90
 Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn
 95 100 105
 Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly
 110 115 120
 Phe Met Val Ser

<210> 347
 <211> 509
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 22
 <223> unknown base
 <400> 347

cacagttccc caccatcact cntcccatc cttccaactt tatttttagc 50
 ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100
 ggagagggac agaggccaga ggactttctca tactggacag aaaccgatca 150
 ggcatggaac tccccttcgt cactcacctg ttcttgcccc tgggtgttct 200
 gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250
 tcccagggcc accagaagct gaatttggat acagtgtctt acaacatgtt 300
 gggggtggac agcgatggat gctgggtggc gccccctggg atgggccttc 350
 aggcgaccgg aggggggacg tttatcgctg ccctgtaggg ggggccaca 400
 atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450
 tctcatcctg ctgtgaatat gcacctggg atgtctctgt tagagacaga 500
 tggatgatgg 509

<210> 348
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 348
 agggacagag gccagaggac ttc 23

 <210> 349
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 349
 caggtgcata ttcacagcag gatg 24

 <210> 350
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 350
 ggaactcccc ttcgtcactc acctgttctt gccccctggg ttct 45

 <210> 351
 <211> 2056
 <212> DNA

<213> Homo sapiens

<400> 351

aaagttacat tttctctgga actctcctag gccactccct gctgatgcaa 50
catctggggtt tgggcagaaa ggagggtgct tcggagcccg ccctttctga 100
gcttcctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200
gctttatttt ggaaagaaac aatgttctag gtcaaactga gtctacaaa 250
tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300
tggtttttct acgcattgat tccatgtttg ctcacagatg aagtggccat 350
tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400
tcttgatgtg gagcccagtg atcgcgcctg gagaaacagt gtactattct 450
gtcgaatacc agggggagta cgagagcctg tacacgagcc acatctggat 500
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atgacatcac ggccactgtg ccatacaacc ttcgtgtcag ggccacattg 600
ggctcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650
ctcaaccatc cttacccgac ctgggatgga gatcaccaa gatggcttcc 700
acctggttat tgagctggag gacctggggc ccagtttga gttccttgtg 750
gcctactgga ggaggagacc tggtgccgag gaacatgtca aaatggtgag 800
gagtgggggt attccagtg acctagaaac catggagcca ggggctgcat 850
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ttcagccaga cagaatgtgt ggagggtgcaa ggagaggcca tccccctgg 950
actggccctg tttgcctttg ttggcttcat gctgatcctt gtggtcgtgc 1000
cactgttcgt ctggaaaatg ggccggctgc tccagtactc ctgttgcccc 1050
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aatcagctgc agaagggagg aggtggatgc ctgtgccacg gctgtgatgt 1150
ctcctgagga actcctcagg gcctggatct cataggtttg cggaagggcc 1200
caggtgaagc cgagaacctg gtctgcatga catggaaacc atgaggggac 1250
aagttgtgtt tctgttttcc gccacggaca agggatgaga gaagtaggaa 1300
gagcctgttg tctacaagtc tagaagcaac catcagaggc agggtggttt 1350
gtctaacaga aactgactg aggcctaggg gatgtgacct ctagactggg 1400

Thr	Ser	Ala	Trp	Ser	Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser	
				125					130					135	
Thr	Ile	Leu	Thr	Arg	Pro	Gly	Met	Glu	Ile	Thr	Lys	Asp	Gly	Phe	
				140					145					150	
His	Leu	Val	Ile	Glu	Leu	Glu	Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe	
				155					160					165	
Leu	Val	Ala	Tyr	Trp	Arg	Arg	Glu	Pro	Gly	Ala	Glu	Glu	His	Val	
				170					175					180	
Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro	Val	His	Leu	Glu	Thr	Met	
				185					190					195	
Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala	Gln	Thr	Phe	Val	Lys	
				200					205					210	
Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr	Glu	Cys	Val	Glu	
				215					220					225	
Val	Gln	Gly	Glu	Ala	Ile	Pro	Leu	Val	Leu	Ala	Leu	Phe	Ala	Phe	
				230					235					240	
Val	Gly	Phe	Met	Leu	Ile	Leu	Val	Val	Val	Pro	Leu	Phe	Val	Trp	
				245					250					255	
Lys	Met	Gly	Arg	Leu	Leu	Gln	Tyr	Ser	Cys	Cys	Pro	Val	Val	Val	
				260					265					270	
Leu	Pro	Asp	Thr	Leu	Lys	Ile	Thr	Asn	Ser	Pro	Gln	Lys	Leu	Ile	
				275					280					285	
Ser	Cys	Arg	Arg	Glu	Glu	Val	Asp	Ala	Cys	Ala	Thr	Ala	Val	Met	
				290					295					300	
Ser	Pro	Glu	Glu	Leu	Leu	Arg	Ala	Trp	Ile	Ser					
				305					310						

<210> 353

<211> 864

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 654, 711, 748, 827

<223> unknown base

<400> 353

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tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150

agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200

ccaaatgcag actttcacaa tggttctaga agaaatctgg acaagtcttt 250
 tcatgtgggt tttctacga ttgattccat gtttgctcac agatgaagtg 300
 gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350
 gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400
 attctgtcga ataccagggg gagtacgaga gcctgtacac gagccacatc 450
 tggatcccca gcagctgggt ctcaactact gaaggtcctg agtgtgatgt 500
 cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550
 cattgggctc acagacctca gcctggagca tcctgaagca tccctttaat 600
 agaaactcaa ccatccttac ccgacctggg atggagatca ccaaagatgg 650
 cttncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700
 ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750
 gaaccccttg cggccgctgg ggtatctctc gagaaaagag agggccaata 800
 tgaccacat actcaatat gacgaantgc tattgtccac ctgtttgagt 850
 ggcgctgggt tgat 864

<210> 354
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 354
 aggcttcgct gcgactagac ctc 23

 <210> 355
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 355
 ccaggtcggg taaggatggt tgag 24

 <210> 356
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

```

<400> 356
  tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357
<211> 1670
<212> DNA
<213> Homo sapiens

<400> 357
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<210> 358
<211> 328
<212> PRT
<213> Homo sapiens

<400> 358
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Pro Glu Asp Trp Trp Ser Tyr Lys Asp Asn Leu Gln Gly Asn Phe
35 40 45
Val Pro Gly Pro Pro Phe Trp Gly Leu Val Asn Ala Ala Trp Ser
50 55 60
Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu
65 70 75
Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser
80 85 90
Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg
95 100 105
His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser
110 115 120
Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu
125 130 135
Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn
140 145 150
His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln
155 160 165
Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly

<220>

<223> Synthetic oligonucleotide probe

<400> 361

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<210> 362

<211> 3038

<212> DNA

<213> Homo sapiens

<400> 362

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gcagctccct tccccccca actgcaggtc taattttgga cgctttgcct 200

gccatttctt ccaggttgag ggagccgcag aggcggaggc tcgcgtattc 250

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catgcagagt attttggacc ttcataataa attacgaagt cagggtgtatc 700

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acttaataac	tgtaaagttt	ttttctgtta	atttaggcat	atagaatatt	2500
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caaatgaatc	tgttaaaaatg	tttgattcct	tgggaatggc	cttaaaaaata	2600

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 aaattgaggt cacatat ttttctgtatc ctggcaaata ctctgcagg 2750
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<210> 363

<211> 500

<212> PRT

<213> Homo sapiens

<400> 363

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				20					25					30
Leu	Leu	Glu	Lys	Leu	Leu	Glu	Lys	Tyr	Met	Asp	Glu	Asp	Gly	Glu
				35					40					45
Trp	Trp	Ile	Ala	Lys	Gln	Arg	Gly	Lys	Arg	Ala	Ile	Thr	Asp	Asn
				50					55					60
Asp	Met	Gln	Ser	Ile	Leu	Asp	Leu	His	Asn	Lys	Leu	Arg	Ser	Gln
				65					70					75
Val	Tyr	Pro	Thr	Ala	Ser	Asn	Met	Glu	Tyr	Met	Thr	Trp	Asp	Val
				80					85					90
Glu	Leu	Glu	Arg	Ser	Ala	Glu	Ser	Trp	Ala	Glu	Ser	Cys	Leu	Trp
				95					100					105
Glu	His	Gly	Pro	Ala	Ser	Leu	Leu	Pro	Ser	Ile	Gly	Gln	Asn	Leu
				110					115					120
Gly	Ala	His	Trp	Gly	Arg	Tyr	Arg	Pro	Pro	Thr	Phe	His	Val	Gln
				125					130					135
Ser	Trp	Tyr	Asp	Glu	Val	Lys	Asp	Phe	Ser	Tyr	Pro	Tyr	Glu	His
				140					145					150
Glu	Cys	Asn	Pro	Tyr	Cys	Pro	Phe	Arg	Cys	Ser	Gly	Pro	Val	Cys
				155					160					165
Thr	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	Thr	Ser	Asn	Arg	Ile	Gly

Val	Asp	Lys	Arg	Lys	Thr	Tyr	Ile	Ala	Ser	Phe	Gln	Asn	Gly	Ile
				470					475					480
Phe	Ser	Glu	Ser	Leu	Gln	Asn	Pro	Pro	Gly	Gly	Lys	Ala	Phe	Arg
				485					490					495
Val	Phe	Ala	Val	Val										
				500										

<210> 364
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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 364
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<210> 365
 <211> 20
 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 365
 ccaagagtat actgtcctcg 20

<210> 366
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 366
 agcacagatt ttctctacag cccc 25

<210> 367
 <211> 24
 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 367
 aaccactcca gcatgtactg ctgc 24

<210> 368
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 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 368

ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369

<211> 1685

<212> DNA

<213> Homo sapiens

<400> 369

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 ataaaatata tttgaaatgt aaaaaaaaaa aaaaa 1685

<210> 370

<211> 111

<212> PRT

<213> Homo sapiens

<400> 370

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Leu	Ala	Ala	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Tyr	Thr	Ala
				20					25					30

Arg	Val	Asp	Gly	Ser	Lys	Cys	Lys	Cys	Ser	Arg	Lys	Gly	Pro	Lys
				35					40					45

Ile	Arg	Tyr	Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro	Lys	Tyr
				50					55					60

Pro	His	Cys	Glu	Glu	Lys	Met	Val	Ile	Ile	Thr	Thr	Lys	Ser	Val
				65					70					75

Ser	Arg	Tyr	Arg	Gly	Gln	Glu	His	Cys	Leu	His	Pro	Lys	Leu	Gln
				80					85					90

Ser	Thr	Lys	Arg	Phe	Ile	Lys	Trp	Tyr	Asn	Ala	Trp	Asn	Glu	Lys
				95					100					105

Arg	Arg	Val	Tyr	Glu	Glu
				110	

<210> 371

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

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<210> 372

<211> 24

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 372

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<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

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<210> 375
<211> 816
<212> PRT
<213> Homo sapiens

<400> 375
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Thr Asn Tyr Gly Lys Ile Arg Gly Leu Arg Thr Pro Leu Pro Asn
35 40 45
Glu Ile Leu Gly Pro Val Glu Gln Tyr Leu Gly Val Pro Tyr Ala

50										55					60				
Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro					
				65					70					75					
Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val					
				80					85					90					
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu					
				95					100					105					
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val					
				110					115					120					
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro					
				125					130					135					
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr					
				140					145					150					
Ser	Asn	Asp	Arg	Gly	Glu	Asp	Glu	Asp	Ile	His	Asp	Gln	Asn	Ser					
				155					160					165					
Lys	Lys	Pro	Val	Met	Val	Tyr	Ile	His	Gly	Gly	Ser	Tyr	Met	Glu					
				170					175					180					
Gly	Thr	Gly	Asn	Met	Ile	Asp	Gly	Ser	Ile	Leu	Ala	Ser	Tyr	Gly					
				185					190					195					
Asn	Val	Ile	Val	Ile	Thr	Ile	Asn	Tyr	Arg	Leu	Gly	Ile	Leu	Gly					
				200					205					210					
Phe	Leu	Ser	Thr	Gly	Asp	Gln	Ala	Ala	Lys	Gly	Asn	Tyr	Gly	Leu					
				215					220					225					
Leu	Asp	Gln	Ile	Gln	Ala	Leu	Arg	Trp	Ile	Glu	Glu	Asn	Val	Gly					
				230					235					240					
Ala	Phe	Gly	Gly	Asp	Pro	Lys	Arg	Val	Thr	Ile	Phe	Gly	Ser	Gly					
				245					250					255					
Ala	Gly	Ala	Ser	Cys	Val	Ser	Leu	Leu	Thr	Leu	Ser	His	Tyr	Ser					
				260					265					270					
Glu	Gly	Leu	Phe	Gln	Lys	Ala	Ile	Ile	Gln	Ser	Gly	Thr	Ala	Leu					
				275					280					285					
Ser	Ser	Trp	Ala	Val	Asn	Tyr	Gln	Pro	Ala	Lys	Tyr	Thr	Arg	Ile					
				290					295					300					
Leu	Ala	Asp	Lys	Val	Gly	Cys	Asn	Met	Leu	Asp	Thr	Thr	Asp	Met					
				305					310					315					
Val	Glu	Cys	Leu	Arg	Asn	Lys	Asn	Tyr	Lys	Glu	Leu	Ile	Gln	Gln					
				320					325					330					
Thr	Ile	Thr	Pro	Ala	Thr	Tyr	His	Ile	Ala	Phe	Gly	Pro	Val	Ile					
				335					340					345					

Asp Gly Asp Val	Ile Pro Asp Asp Pro	Gln Ile Leu Met Glu Gln	350	355	360
Gly Glu Phe Leu	Asn Tyr Asp Ile Met	Leu Gly Val Asn Gln Gly	365	370	375
Glu Gly Leu Lys	Phe Val Asp Gly Ile	Val Asp Asn Glu Asp Gly	380	385	390
Val Thr Pro Asn	Asp Phe Asp Phe Ser	Val Ser Asn Phe Val Asp	395	400	405
Asn Leu Tyr Gly	Tyr Pro Glu Gly Lys	Asp Thr Leu Arg Glu Thr	410	415	420
Ile Lys Phe Met	Tyr Thr Asp Trp Ala	Asp Lys Glu Asn Pro Glu	425	430	435
Thr Arg Arg Lys	Thr Leu Val Ala Leu	Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly Ser	455	460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn	Phe Ala Lys Thr Gly	Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn Leu	590	595	600
Asn Glu Ile Phe	Gln Tyr Val Ser Thr	Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala Asn			

635					640					645				
Asn	Pro	Lys	His	Ser	Lys	Asp	Pro	His	Lys	Thr	Gly	Pro	Glu	Asp
				650					655					660
Thr	Thr	Val	Leu	Ile	Glu	Thr	Lys	Arg	Asp	Tyr	Ser	Thr	Glu	Leu
				665					670					675
Ser	Val	Thr	Ile	Ala	Val	Gly	Ala	Ser	Leu	Leu	Phe	Leu	Asn	Ile
				680					685					690
Leu	Ala	Phe	Ala	Ala	Leu	Tyr	Tyr	Lys	Lys	Asp	Lys	Arg	Arg	His
				695					700					705
Glu	Thr	His	Arg	Arg	Pro	Ser	Pro	Gln	Arg	Asn	Thr	Thr	Asn	Asp
				710					715					720
Ile	Ala	His	Ile	Gln	Asn	Glu	Glu	Ile	Met	Ser	Leu	Gln	Met	Lys
				725					730					735
Gln	Leu	Glu	His	Asp	His	Glu	Cys	Glu	Ser	Leu	Gln	Ala	His	Asp
				740					745					750
Thr	Leu	Arg	Leu	Thr	Cys	Pro	Pro	Asp	Tyr	Thr	Leu	Thr	Leu	Arg
				755					760					765
Arg	Ser	Pro	Asp	Asp	Ile	Pro	Leu	Met	Thr	Pro	Asn	Thr	Ile	Thr
				770					775					780
Met	Ile	Pro	Asn	Thr	Leu	Thr	Gly	Met	Gln	Pro	Leu	His	Thr	Phe
				785					790					795
Asn	Thr	Phe	Ser	Gly	Gly	Gln	Asn	Ser	Thr	Asn	Leu	Pro	His	Gly
				800					805					810
His	Ser	Thr	Thr	Arg	Val									
				815										

<210> 376

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 376

ggcaagctac ggaaacgtca tcgtg 25

<210> 377

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 377

aacccccgag ccaaaagatg gtcac 25

<210> 378

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 378

gtaccggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

gggaaagatg gcggcgactc tgggaccct tgggtcgtgg cagcagtggc 50

ggcgatgttt gtcggctcgg gatgggtcca ggatgttact cttcttctt 100

ttgttggggc ctgggcaggg gccacagcaa gtcggggcgg gtcaaacgtt 150

cgagtacttg aaacgggagc actcgctgtc gaagccctac cagggtgtgg 200

gcacaggcag ttcctcactg tggaatctga tgggcaatgc catggtgatg 250

accagttata tccgccttac ccagatatg caaagtaaac aggggtgcctt 300

gtggaaccgg gtgccatgtt tcctgagaga ctgggagttg cagggtgcact 350

tcaaaatcca tggacaagga aagaagaatc tgcattggga tggcttggca 400

atctggtaca caaaggatcg gatgcagcca gggcctgtgt ttggaaacat 450

ggacaaatth gtggggctgg gagtatttgt agacacctac cccaatgagg 500

agaagcagca agagcgggta tccccctaca tctcagccat ggtgaacaac 550

ggctccctca gctatgatca tgagcgggat gggcggccta cagagctggg 600

aggctgcaca gccattgtcc gcaatcttca ttacgacacc ttcctggtga 650

ttcgctacgt caagaggcat ttgacgataa tgatggatat tgatggcaag 700

catgagtgga gggactgcat tgaagtgccg ggagtccgcc tgccccgcgg 750

ctactacttc ggcacctcct ccatcactgg ggatctctca gataatcatg 800

atgtcatttc cttgaagttg tttgaactga cagtggagag aaccccagaa 850

gaggaaaagc tccatcgaga tgtgttcttg ccctcagtgg acaatatgaa 900

gctgcctgag atgacagctc cactgccgcc cctgagtggc ctggccctct 950

tcctcatcgt ctttttctcc ctggtgtttt ctgtatttgc catagtcatt 1000

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 gaccccgcat tcccatgggt gtgcatgggg acatctaact ctggtctggg 1250
 aagccacca cccagggca atgctgctgt gatgtgcctt tccctgcagt 1300
 ccttccatgt gggagcagag gtgtgaagag aatttacgtg gttgtgatgc 1350
 caaaatcaca gaacagaatt tcatagccca ggctgccgtg ttgtttgact 1400
 cagaaggccc ttctacttca gttttgaatc cacaagaat taaaaactgg 1450
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 cttggagggc ctggaactct gagtcctcct atgaacctct gtagcctaaa 2350
 tgaaattctt aaaatcaccg atggaaccaa aaaaaaaaaa aaaaaggcgc 2400
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ggccgccatg g 2461

<210> 380

<211> 348

<212> PRT

<213> Homo sapiens

<400> 380

Met Ala Ala Thr Leu Gly Pro Leu Gly Ser Trp Gln Gln Trp Arg
1 5 10 15

Arg Cys Leu Ser Ala Arg Asp Gly Ser Arg Met Leu Leu Leu Leu
20 25 30

Leu Leu Leu Gly Ser Gly Gln Gly Pro Gln Gln Val Gly Ala Gly
35 40 45

Gln Thr Phe Glu Tyr Leu Lys Arg Glu His Ser Leu Ser Lys Pro
50 55 60

Tyr Gln Gly Val Gly Thr Gly Ser Ser Ser Leu Trp Asn Leu Met
65 70 75

Gly Asn Ala Met Val Met Thr Gln Tyr Ile Arg Leu Thr Pro Asp
80 85 90

Met Gln Ser Lys Gln Gly Ala Leu Trp Asn Arg Val Pro Cys Phe
95 100 105

Leu Arg Asp Trp Glu Leu Gln Val His Phe Lys Ile His Gly Gln
110 115 120

Gly Lys Lys Asn Leu His Gly Asp Gly Leu Ala Ile Trp Tyr Thr
125 130 135

Lys Asp Arg Met Gln Pro Gly Pro Val Phe Gly Asn Met Asp Lys
140 145 150

Phe Val Gly Leu Gly Val Phe Val Asp Thr Tyr Pro Asn Glu Glu
155 160 165

Lys Gln Gln Glu Arg Val Phe Pro Tyr Ile Ser Ala Met Val Asn
170 175 180

Asn Gly Ser Leu Ser Tyr Asp His Glu Arg Asp Gly Arg Pro Thr
185 190 195

Glu Leu Gly Gly Cys Thr Ala Ile Val Arg Asn Leu His Tyr Asp
200 205 210

Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His Leu Thr Ile Met
215 220 225

Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys Ile Glu Val
230 235 240

Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr Ser Ser
245 250 255

Ile Thr Gly Asp	Leu Ser Asp Asn His	Asp Val Ile Ser Leu Lys
260	265	270
Leu Phe Glu Leu Thr Val Glu Arg Thr	Pro Glu Glu Glu Lys Leu	
275	280	285
His Arg Asp Val Phe Leu Pro Ser Val	Asp Asn Met Lys Leu Pro	
290	295	300
Glu Met Thr Ala Pro Leu Pro Pro Leu	Ser Gly Leu Ala Leu Phe	
305	310	315
Leu Ile Val Phe Phe Ser Leu Val Phe	Ser Val Phe Ala Ile Val	
320	325	330
Ile Gly Ile Ile Leu Tyr Asn Lys Trp	Gln Glu Gln Ser Arg Lys	
335	340	345

Arg Phe Tyr

<210> 381

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 381

ccttggtcg tggcagcagt gg 22

<210> 382

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 382

cactctccag gctgcatgct cagg 24

<210> 383

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 383

gtcaaacgtt cgagtacttg aaacgggagc actcgtgtc gaagc 45

<210> 384

<211> 3150

<212> DNA

<213> Homo sapiens

<400> 384

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gtgagtgcaa tctacggatc agtctctgat ggtgggtcgt taacctcagt 100
ggggactcca agatttccat gaagaaaatc agttgtcttc attcaagaat 150
tggggtcttg ctcagaatc ctgcagctgg tgaaaatctg ttttctagaa 200
gaggtttaat taatgcctgc agtctgacat gttcccgatt tgaggtgaaa 250
ccatgaagag aaaatagaat acttaataat gcttttccgc aaccgcttct 300
tgctgtgctt ggccctggct gcgctgctgg cctttgtgag cctcagcctg 350
cagttcttcc acctgatccc ggtgtcgact cctaagaatg gaatgagtag 400
caagagtoga aagagaatca tgcccgaccc tgtgacggag cccctgtga 450
cagaccccgt ttatgaagct cttttgtact gcaacatccc cagtgtggcc 500
gagcgcagca tggaaggtea tgcccgcat catTTtaagc tggTctcagt 550
gcatgtgttc attcgccacg gagacaggta cccactgtat gtcattccca 600
aaacaaagcg accagaaatt gactgcactc tggTggctaa caggaaaccg 650
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agcctctttc gaaagccct tgaactcctt gcctctttac ccaaTcacc 750
cattgtgtga gatgggagag ctcacacaga caggagtTgt gcagcatttg 800
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gccggaccct acaaagtggg ctggccttgc tttatggctt tctccagat 950
tttgactgga agaagattta tttcaggcac cagccaagtg cgctgtTctg 1000
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agcgtcgtca gtacctcta cgtttgaaaa acagccagct ggagaagacc 1100
tacggggaga tggccaagat cgtggatgtc cccaccaagc agcttagagc 1150
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aagaccatc agatcgagga tgaaagggaa agacgggaga agaaattgta 1300
cttcgggtat tctctcctgg gtgccaccc catcctgaac caaaccatcg 1350
gccggatgca gcgtgccacc gagggcagga aagaagagct ctttgccctc 1400
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ttcagaagcc aggttcccaa ggtttgcagc caggttgatc tttgagcttt 1500
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 ggcgtcgatg tcacattcca cacctctttc tgccaagacc accacaagcg 1600
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 atgccaatac agagcatagg gaaagggtcca cttctagttt tgtctgttac 1800
 taagggtaga agattattgc tttttaagg ctaaattattg tttgtgggaa 1850
 ccacagatgg ttgggggtga acagtaagca cattgctgca atgtggtacg 1900
 tgaattgctt ggtacaaaat ggccagttca cagaggaata gaaggactt 1950
 tatcatagcc agacttcgct tagaatgcca gaataatata gttcaagacc 2000
 tgaagttgcc aatccaagtt tgcaactctc tggcctgccc catgttacta 2050
 tgtgatggaa ccagcacacc tcaacaaaaa tttttttaat cttagacatt 2100
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 ggttggcaaa ctttttctgt aaagggccag attgtaaata tttcagactg 2200
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 ttctgaagca ggaaagccac cacagacagt acataaagga atatgtgtag 2300
 ctgggttccc aggccagaca aaacagatgg tgaccagact tggcccctgg 2350
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 acttccagca ctttgagaac gagttgaata ccaagaatta ttcaatggtt 2450
 cctccagtaa cttctgctag aaacacagaa tttggtctgt atctgacact 2500
 agaacaaaac ttgagggtaa ataaacattg aattagaatg aatcatagaa 2550
 aactgattag aagaatactt gatgtttatg atgattgtgg tacaagatag 2600
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 tgatttctga actaatgggtg ctaattcaga gaaatggaaa gtgaaagtga 3050
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<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

Met	Leu	Phe	Arg	Asn	Arg	Phe	Leu	Leu	Leu	Leu	Ala	Leu	Ala	Ala	1	5	10	15
Leu	Leu	Ala	Phe	Val	Ser	Leu	Ser	Leu	Gln	Phe	Phe	His	Leu	Ile	20	25	30	
Pro	Val	Ser	Thr	Pro	Lys	Asn	Gly	Met	Ser	Ser	Lys	Ser	Arg	Lys	35	40	45	
Arg	Ile	Met	Pro	Asp	Pro	Val	Thr	Glu	Pro	Pro	Val	Thr	Asp	Pro	50	55	60	
Val	Tyr	Glu	Ala	Leu	Leu	Tyr	Cys	Asn	Ile	Pro	Ser	Val	Ala	Glu	65	70	75	
Arg	Ser	Met	Glu	Gly	His	Ala	Pro	His	His	Phe	Lys	Leu	Val	Ser	80	85	90	
Val	His	Val	Phe	Ile	Arg	His	Gly	Asp	Arg	Tyr	Pro	Leu	Tyr	Val	95	100	105	
Ile	Pro	Lys	Thr	Lys	Arg	Pro	Glu	Ile	Asp	Cys	Thr	Leu	Val	Ala	110	115	120	
Asn	Arg	Lys	Pro	Tyr	His	Pro	Lys	Leu	Glu	Ala	Phe	Ile	Ser	His	125	130	135	
Met	Ser	Lys	Gly	Ser	Gly	Ala	Ser	Phe	Glu	Ser	Pro	Leu	Asn	Ser	140	145	150	
Leu	Pro	Leu	Tyr	Pro	Asn	His	Pro	Leu	Cys	Glu	Met	Gly	Glu	Leu	155	160	165	
Thr	Gln	Thr	Gly	Val	Val	Gln	His	Leu	Gln	Asn	Gly	Gln	Leu	Leu	170	175	180	
Arg	Asp	Ile	Tyr	Leu	Lys	Lys	His	Lys	Leu	Leu	Pro	Asn	Asp	Trp	185	190	195	
Ser	Ala	Asp	Gln	Leu	Tyr	Leu	Glu	Thr	Thr	Gly	Lys	Ser	Arg	Thr	200	205	210	

Leu	Gln	Ser	Gly	Leu	Ala	Leu	Leu	Tyr	Gly	Phe	Leu	Pro	Asp	Phe
				215					220					225
Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe
				230					235					240
Cys	Ser	Gly	Ser	Cys	Tyr	Cys	Pro	Val	Arg	Asn	Gln	Tyr	Leu	Glu
				245					250					255
Lys	Glu	Gln	Arg	Arg	Gln	Tyr	Leu	Leu	Arg	Leu	Lys	Asn	Ser	Gln
				260					265					270
Leu	Glu	Lys	Thr	Tyr	Gly	Glu	Met	Ala	Lys	Ile	Val	Asp	Val	Pro
				275					280					285
Thr	Lys	Gln	Leu	Arg	Ala	Ala	Asn	Pro	Ile	Asp	Ser	Met	Leu	Cys
				290					295					300
His	Phe	Cys	His	Asn	Val	Ser	Phe	Pro	Cys	Thr	Arg	Asn	Gly	Cys
				305					310					315
Val	Asp	Met	Glu	His	Phe	Lys	Val	Ile	Lys	Thr	His	Gln	Ile	Glu
				320					325					330
Asp	Glu	Arg	Glu	Arg	Arg	Glu	Lys	Lys	Leu	Tyr	Phe	Gly	Tyr	Ser
				335					340					345
Leu	Leu	Gly	Ala	His	Pro	Ile	Leu	Asn	Gln	Thr	Ile	Gly	Arg	Met
				350					355					360
Gln	Arg	Ala	Thr	Glu	Gly	Arg	Lys	Glu	Glu	Leu	Phe	Ala	Leu	Tyr
				365					370					375
Ser	Ala	His	Asp	Val	Thr	Leu	Ser	Pro	Val	Leu	Ser	Ala	Leu	Gly
				380					385					390
Leu	Ser	Glu	Ala	Arg	Phe	Pro	Arg	Phe	Ala	Ala	Arg	Leu	Ile	Phe
				395					400					405
Glu	Leu	Trp	Gln	Asp	Arg	Glu	Lys	Pro	Ser	Glu	His	Ser	Val	Arg
				410					415					420
Ile	Leu	Tyr	Asn	Gly	Val	Asp	Val	Thr	Phe	His	Thr	Ser	Phe	Cys
				425					430					435
Gln	Asp	His	His	Lys	Arg	Ser	Pro	Lys	Pro	Met	Cys	Pro	Leu	Glu
				440					445					450
Asn	Leu	Val	Arg	Phe	Val	Lys	Arg	Asp	Met	Phe	Val	Ala	Leu	Gly
				455					460					465
Gly	Ser	Gly	Thr	Asn	Tyr	Tyr	Asp	Ala	Cys	His	Arg	Glu	Gly	Phe
				470					475					480

<210> 386

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 386
ccaagcagct tagagctcca gacc 24

<210> 387
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 387
ttccctatgc tctgtattgg catgg 25

<210> 388
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
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<400> 388
gccacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtgtt 50

<210> 389
<211> 3313
<212> DNA
<213> Homo sapiens

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gccgctgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200
cacgcgcctg aagcaciaag cagatagcta ggaatgaacc atccctggga 250
gtatgtggaa acaacggagg agctctgact tcccaactgt cccattctat 300
gggcgaagga actgctcctg acttcagtgg ttaagggcag aattgaaaat 350
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atgcacccag atacgctatt cagttccgga agagctggag aaaggctcta 500
gggtgggcga catctccagg gacctggggc tggagccccg ggagctcgcg 550
gagcgcggag tccgcatcat ccccagaggt aggacgcagc ttttcgccct 600

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 aaactctatc tca 3313

<210> 390
 <211> 916
 <212> PRT
 <213> Homo sapiens
 <400> 390

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Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val	35	40	45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala	50	55	60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe	65	70	75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile	80	85	90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn	95	100	105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu	110	115	120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu	125	130	135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met	140	145	150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn	155	160	165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu	170	175	180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val	185	190	195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu	200	205	210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr	215	220	225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	230	235	240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu	245	250	255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp	260	265	270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp	275	280	285	
Asp	Lys	Ala	Ala	Gln	Val	Phe	Lys	Leu	Asp	Cys	Asn	Ser	Gly	Thr				

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Ile Ser Thr Ile	Gly 305	Glu Leu Asp His	Glu 310	Glu Ser Gly Phe	Tyr 315
Gln Met Glu Val	Gln 320	Ala Met Asp Asn	Ala 325	Gly Tyr Ser Ala	Arg 330
Ala Lys Val Leu	Ile 335	Thr Val Leu Asp	Val 340	Asn Asp Asn Ala	Pro 345
Glu Val Val Leu	Thr 350	Ser Leu Ala Ser	Ser 355	Val Pro Glu Asn	Ser 360
Pro Arg Gly Thr	Leu 365	Ile Ala Leu Leu	Asn 370	Val Asn Asp Gln	Asp 375
Ser Glu Glu Asn	Gly 380	Gln Val Ile Cys	Phe 385	Ile Gln Gly Asn	Leu 390
Pro Phe Lys Leu	Glu 395	Lys Ser Tyr Gly	Asn 400	Tyr Tyr Ser Leu	Val 405
Thr Asp Ile Val	Leu 410	Asp Arg Glu Gln	Val 415	Pro Ser Tyr Asn	Ile 420
Thr Val Thr Ala	Thr 425	Asp Arg Gly Thr	Pro 430	Pro Leu Ser Thr	Glu 435
Thr His Ile Ser	Leu 440	Asn Val Ala Asp	Thr 445	Asn Asp Asn Pro	Pro 450
Val Phe Pro Gln	Ala 455	Ser Tyr Ser Ala	Tyr 460	Ile Pro Glu Asn	Asn 465
Pro Arg Gly Val	Ser 470	Leu Val Ser Val	Thr 475	Ala His Asp Pro	Asp 480
Cys Glu Glu Asn	Ala 485	Gln Ile Thr Tyr	Ser 490	Leu Ala Glu Asn	Thr 495
Ile Gln Gly Ala	Ser 500	Leu Ser Ser Tyr	Val 505	Ser Ile Asn Ser	Asp 510
Thr Gly Val Leu	Tyr 515	Ala Leu Ser Ser	Phe 520	Asp Tyr Glu Gln	Phe 525
Arg Asp Leu Gln	Val 530	Lys Val Met Ala	Arg 535	Asp Asn Gly His	Pro 540
Pro Leu Ser Ser	Asn 545	Val Ser Leu Ser	Leu 550	Phe Val Leu Asp	Gln 555
Asn Asp Asn Ala	Pro 560	Glu Ile Leu Tyr	Pro 565	Ala Leu Pro Thr	Asp 570
Gly Ser Thr Gly	Val 575	Glu Leu Ala Pro	Arg 580	Ser Ala Glu Pro	Gly 585

Tyr	Leu	Val	Thr	Lys	Val	Val	Ala	Val	Asp	Arg	Asp	Ser	Gly	Gln	590	595	600
Asn	Ala	Trp	Leu	Ser	Tyr	Arg	Leu	Leu	Lys	Ala	Ser	Glu	Pro	Gly	605	610	615
Leu	Phe	Ser	Val	Gly	Leu	His	Thr	Gly	Glu	Val	Arg	Thr	Ala	Arg	620	625	630
Ala	Leu	Leu	Asp	Arg	Asp	Ala	Leu	Lys	Gln	Ser	Leu	Val	Val	Ala	635	640	645
Val	Gln	Asp	His	Gly	Gln	Pro	Pro	Leu	Ser	Ala	Thr	Val	Thr	Leu	650	655	660
Thr	Val	Ala	Val	Ala	Asp	Ser	Ile	Pro	Gln	Val	Leu	Ala	Asp	Leu	665	670	675
Gly	Ser	Leu	Glu	Ser	Pro	Ala	Asn	Ser	Glu	Thr	Ser	Asp	Leu	Thr	680	685	690
Leu	Tyr	Leu	Val	Val	Ala	Val	Ala	Ala	Val	Ser	Cys	Val	Phe	Leu	695	700	705
Ala	Phe	Val	Ile	Leu	Leu	Leu	Ala	Leu	Arg	Leu	Arg	Arg	Trp	His	710	715	720
Lys	Ser	Arg	Leu	Leu	Gln	Ala	Ser	Gly	Gly	Gly	Leu	Thr	Gly	Ala	725	730	735
Pro	Ala	Ser	His	Phe	Val	Gly	Val	Asp	Gly	Val	Gln	Ala	Phe	Leu	740	745	750
Gln	Thr	Tyr	Ser	His	Glu	Val	Ser	Leu	Thr	Thr	Asp	Ser	Arg	Lys	755	760	765
Ser	His	Leu	Ile	Phe	Pro	Gln	Pro	Asn	Tyr	Ala	Asp	Met	Leu	Val	770	775	780
Ser	Gln	Glu	Ser	Phe	Glu	Lys	Ser	Glu	Pro	Leu	Leu	Leu	Ser	Gly	785	790	795
Asp	Ser	Val	Phe	Ser	Lys	Asp	Ser	His	Gly	Leu	Ile	Glu	Val	Ser	800	805	810
Leu	Tyr	Gln	Ile	Phe	Phe	Leu	Phe	Phe	Phe	Asn	Cys	Ser	Val	Ser	815	820	825
Gln	Ala	Gly	Val	Gln	Arg	Tyr	Asp	His	Ser	Ser	Leu	Arg	Pro	Gln	830	835	840
Thr	Pro	Arg	Leu	Lys	Gln	Leu	Ser	His	Leu	Cys	Leu	Arg	Cys	Asn	845	850	855
Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr	860	865	870
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu			

	875		880		885
Ser Cys Thr Asp Gly Ser Leu Thr Pro Val Ile Pro Val Leu Trp					
	890		895		900
Glu Ala Glu Ala Gly Gly Ser Pro Glu Val Gly Ser Leu Arg Pro					
	905		910		915

Ala

<210> 391
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

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<210> 392
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 392
 ctcgggcgca ttgtcgttct ggtc 24

<210> 393
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 393
 ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

<210> 394
 <211> 999
 <212> DNA
 <213> Homo sapiens

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 ggggcctcct ccaactgggtc cgaatcagta ggtgaccccg cccctggatt 150
 ctggaagacc tcaccatggg acgccccga cctcgtgcgg ccaagacgtg 200

gatgttcctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250
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tggcaggcgg ccttggtcca gggccagcaa ctactctgtg gcggtgtcct 350
tgtaggtggc aactgggtcc ttacagctgc ccactgtaaa aaaccgaaat 400
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ctaggataag cactagatct cccttaataa actcacaact ctctggttc 999

<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

Met	Gly	Arg	Pro	Arg	Pro	Arg	Ala	Ala	Lys	Thr	Trp	Met	Phe	Leu
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Leu	Leu	Leu	Gly	Gly	Ala	Trp	Ala	Gly	His	Ser	Arg	Ala	Gln	Glu
			20						25					30
Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
			35						40					45
Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
			50						55					60
Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
			65						70					75
Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn
			80						85					90
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro
			95						100					105

His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp
				110					115					120
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys
				125					130					135
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln
				140					145					150
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu
				155					160					165
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro
				170					175					180
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly
				185					190					195
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly
				200					205					210
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile
				215					220					225
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly
				230					235					240
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile
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Ile	Gly	Ser	Lys	Gly										
				260										

<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

cagcctacag aataaagatg gcc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaatacct gtggttcagt ccataccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

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cgccgcgagg ccccgcccc gcccgcctcc gcccgcccc ggccggcggg 200
ggaaccgggc ggattcctcg cgcgtcaaac cacctgatcc cataaaacat 250
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cccaaccctt acgatgaaga gggcgctccg tggagggagc cggctgctgg 550
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ttacaggggt cggcggcagc gtttgttcca gaacgccgcc tcccaccag 2150
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gacgacgtgg aataaagagc tcttttotta aaaaaa 2236

<210> 400
<211> 473
<212> PRT
<213> Homo sapiens

<400> 400
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Leu Trp Leu Gln Ala Trp Gln Val Ala Ala Pro Cys Pro Gly Ala
20 25 30

Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln	35	40	45
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln	50	55	60
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala	65	70	75
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser	80	85	90
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala	95	100	105
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser	110	115	120
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu	125	130	135
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe	140	145	150
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala	155	160	165
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu	170	175	180
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu	185	190	195
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His	200	205	210
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu	215	220	225
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala	230	235	240
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu	245	250	255
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro	260	265	270
Leu	Trp	Ala	Trp	Leu	Gln	Lys	Phe	Arg	Gly	Ser	Ser	Ser	Glu	Val	275	280	285
Pro	Cys	Ser	Leu	Pro	Gln	Arg	Leu	Ala	Gly	Arg	Asp	Leu	Lys	Arg	290	295	300
Leu	Ala	Ala	Asn	Asp	Leu	Gln	Gly	Cys	Ala	Val	Ala	Thr	Gly	Pro	305	310	315
Tyr	His	Pro	Ile	Trp	Thr	Gly	Arg	Ala	Thr	Asp	Glu	Glu	Pro	Leu			

320	325	330
Gly Leu Pro Lys Cys Cys Gln Pro Asp	Ala Ala Asp Lys Ala Ser	
335	340	345
Val Leu Glu Pro Gly Arg Pro Ala Ser	Ala Gly Asn Ala Leu Lys	
350	355	360
Gly Arg Val Pro Pro Gly Asp Ser Pro	Pro Gly Asn Gly Ser Gly	
365	370	375
Pro Arg His Ile Asn Asp Ser Pro Phe	Gly Thr Leu Pro Gly Ser	
380	385	390
Ala Glu Pro Pro Leu Thr Ala Val Arg	Pro Glu Gly Ser Glu Pro	
395	400	405
Pro Gly Phe Pro Thr Ser Gly Pro Arg	Arg Arg Pro Gly Cys Ser	
410	415	420
Arg Lys Asn Arg Thr Arg Ser His Cys	Arg Leu Gly Gln Ala Gly	
425	430	435
Ser Gly Gly Gly Gly Thr Gly Asp Ser	Glu Gly Ser Gly Ala Leu	
440	445	450
Pro Ser Leu Thr Cys Ser Leu Thr Pro	Leu Gly Leu Ala Leu Val	
455	460	465
Leu Trp Thr Val Leu Gly Pro Cys		
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<211> 24

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

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<210> 402

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 402

ccctgcaggt cattggcagc tagg 24

<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 403

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<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

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agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgaga 200
caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250
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aggatctgtg cggtcacaca gagccctgtg tgctacgttt ccaagtgttg 500
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gatttcctat tcaacttttc aagcttcaga agagattggc aaaaccttta 1050
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tgttttaaag tgaacattta cctttattcc tggttctt 2738

<210> 405
<211> 798
<212> PRT
<213> Homo sapiens

<400> 405

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Phe	Ser	Phe	Leu	Leu	Leu	Gly	Leu	Ser	Leu	Ala	Gly	Ala	Ala	Glu	20	25	30	
Pro	Arg	Ser	Tyr	Ser	Val	Val	Glu	Glu	Thr	Glu	Gly	Ser	Ser	Phe	35	40	45	
Val	Thr	Asn	Leu	Ala	Lys	Asp	Leu	Gly	Leu	Glu	Gln	Arg	Glu	Phe	50	55	60	
Ser	Arg	Arg	Gly	Val	Arg	Val	Val	Ser	Arg	Gly	Asn	Lys	Leu	His	65	70	75	
Leu	Gln	Leu	Asn	Gln	Glu	Thr	Ala	Asp	Leu	Leu	Leu	Asn	Glu	Lys	80	85	90	
Leu	Asp	Arg	Glu	Asp	Leu	Cys	Gly	His	Thr	Glu	Pro	Cys	Val	Leu	95	100	105	
Arg	Phe	Gln	Val	Leu	Leu	Glu	Ser	Pro	Phe	Glu	Phe	Phe	Gln	Ala	110	115	120	
Glu	Leu	Gln	Val	Ile	Asp	Ile	Asn	Asp	His	Ser	Pro	Val	Phe	Leu	125	130	135	
Asp	Lys	Gln	Met	Leu	Val	Lys	Val	Ser	Glu	Ser	Ser	Pro	Pro	Gly	140	145	150	
Thr	Thr	Phe	Pro	Leu	Lys	Asn	Ala	Glu	Asp	Leu	Asp	Val	Gly	Gln	155	160	165	
Asn	Asn	Ile	Glu	Asn	Tyr	Ile	Ile	Ser	Pro	Asn	Ser	Tyr	Phe	Arg	170	175	180	
Val	Leu	Thr	Arg	Lys	Arg	Ser	Asp	Gly	Arg	Lys	Tyr	Pro	Glu	Leu	185	190	195	
Val	Leu	Asp	Lys	Ala	Leu	Asp	Arg	Glu	Glu	Glu	Ala	Glu	Leu	Arg	200	205	210	
Leu	Thr	Leu	Thr	Ala	Leu	Asp	Gly	Gly	Ser	Pro	Pro	Arg	Ser	Gly	215	220	225	
Thr	Ala	Gln	Val	Tyr	Ile	Glu	Val	Leu	Asp	Val	Asn	Asp	Asn	Ala				

Pro Glu Phe Glu Gln	Pro Phe Tyr Arg	Val Gln Ile Ser Glu Asp
245		255
Ser Pro Val Gly Phe	Leu Val Val Lys	Val Ser Ala Thr Asp Val
260		270
Asp Thr Gly Val Asn	Gly Glu Ile Ser	Tyr Ser Leu Phe Gln Ala
275		285
Ser Glu Glu Ile Gly	Lys Thr Phe Lys	Ile Asn Pro Leu Thr Gly
290		300
Glu Ile Glu Leu Lys	Lys Gln Leu Asp	Phe Glu Lys Leu Gln Ser
305		315
Tyr Glu Val Asn Ile	Glu Ala Arg Asp	Ala Gly Thr Phe Ser Gly
320		330
Lys Cys Thr Val Leu	Ile Gln Val Ile	Asp Val Asn Asp His Ala
335		345
Pro Glu Val Thr Met	Ser Ala Phe Thr	Ser Pro Ile Pro Glu Asn
350		360
Ala Pro Glu Thr Val	Val Ala Leu Phe	Ser Val Ser Asp Leu Asp
365		375
Ser Gly Glu Asn Gly	Lys Ile Ser Cys	Ser Ile Gln Glu Asp Leu
380		390
Pro Phe Leu Leu Lys	Ser Ala Glu Asn	Phe Tyr Thr Leu Leu Thr
395		405
Glu Arg Pro Leu Asp	Arg Glu Ser Arg	Ala Glu Tyr Asn Ile Thr
410		420
Ile Thr Val Thr Asp	Leu Gly Thr Pro	Met Leu Ile Thr Gln Leu
425		435
Asn Met Thr Val Leu	Ile Ala Asp Val	Asn Asp Asn Ala Pro Ala
440		450
Phe Thr Gln Thr Ser	Tyr Thr Leu Phe	Val Arg Glu Asn Asn Ser
455		465
Pro Ala Leu His Ile	Arg Ser Val Ser	Ala Thr Asp Arg Asp Ser
470		480
Gly Thr Asn Ala Gln	Val Thr Tyr Ser	Leu Leu Pro Pro Gln Asp
485		495
Pro His Leu Pro Leu	Thr Ser Leu Val	Ser Ile Asn Ala Asp Asn
500		510
Gly His Leu Phe Ala	Leu Arg Ser Leu	Asp Tyr Glu Ala Leu Gln
515		525

Gly	Phe	Gln	Phe	Arg	Val	Gly	Ala	Ser	Asp	His	Gly	Ser	Pro	Ala	
				530					535					540	
Leu	Ser	Ser	Glu	Ala	Leu	Val	Arg	Val	Val	Val	Leu	Asp	Ala	Asn	
				545					550					555	
Asp	Asn	Ser	Pro	Phe	Val	Leu	Tyr	Pro	Leu	Gln	Asn	Gly	Ser	Ala	
				560					565					570	
Pro	Cys	Thr	Glu	Leu	Val	Pro	Arg	Ala	Ala	Glu	Pro	Gly	Tyr	Leu	
				575					580					585	
Val	Thr	Lys	Val	Val	Ala	Val	Asp	Gly	Asp	Ser	Gly	Gln	Asn	Ala	
				590					595					600	
Trp	Leu	Ser	Tyr	Gln	Leu	Leu	Lys	Ala	Thr	Glu	Leu	Gly	Leu	Phe	
				605					610					615	
Gly	Val	Trp	Ala	His	Asn	Gly	Glu	Val	Arg	Thr	Ala	Arg	Leu	Leu	
				620					625					630	
Ser	Glu	Arg	Asp	Ala	Ala	Lys	His	Arg	Leu	Val	Val	Leu	Val	Lys	
				635					640					645	
Asp	Asn	Gly	Glu	Pro	Pro	Arg	Ser	Ala	Thr	Ala	Thr	Leu	His	Val	
				650					655					660	
Leu	Leu	Val	Asp	Gly	Phe	Ser	Gln	Pro	Tyr	Leu	Pro	Leu	Pro	Glu	
				665					670					675	
Ala	Ala	Pro	Thr	Gln	Ala	Gln	Ala	Asp	Leu	Leu	Thr	Val	Tyr	Leu	
				680					685					690	
Val	Val	Ala	Leu	Ala	Ser	Val	Ser	Ser	Leu	Phe	Leu	Phe	Ser	Val	
				695					700					705	
Leu	Leu	Phe	Val	Ala	Val	Arg	Leu	Cys	Arg	Arg	Ser	Arg	Ala	Ala	
				710					715					720	
Ser	Val	Gly	Arg	Cys	Leu	Val	Pro	Glu	Gly	Pro	Leu	Pro	Gly	His	
				725					730					735	
Leu	Val	Asp	Met	Ser	Gly	Thr	Arg	Thr	Leu	Ser	Gln	Ser	Tyr	Gln	
				740					745					750	
Tyr	Glu	Val	Cys	Leu	Ala	Gly	Gly	Ser	Gly	Thr	Asn	Glu	Phe	Lys	
				755					760					765	
Phe	Leu	Lys	Pro	Ile	Ile	Pro	Asn	Phe	Pro	Pro	Gln	Cys	Pro	Gly	
				770					775					780	
Lys	Glu	Ile	Gln	Gly	Asn	Ser	Thr	Phe	Pro	Asn	Asn	Phe	Gly	Phe	
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Asn	Ile	Gln													

<210> 406

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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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ctgagaacgc gcctgaaact gtg 23

<210> 407
<211> 22
<212> DNA
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<220>
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<400> 407
agcgttgtca ttgacatcgg cg 22

<210> 408
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<212> DNA
<213> Artificial Sequence

<220>
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ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409
<211> 1379
<212> DNA
<213> Homo sapiens

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cggtcgacga ccgccccgcg tcatgcggct cctcggctgg tggcaagtat 150
tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200
agtggtcgct tatggtcaga ggagcagcct gtcaccctc tccaggtggg 250
ggctgtgtac ctgggtgagg aggagctcct gcatgaccgc atggggccagg 300
acagggcagc agaagaggcc aatgcggtgc tggggctgga cacccaaggc 350
gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400
gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450
caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500

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tatgctacca	ttcgaactga	gagtattcgg	tggctaattc	caggacaaga	1150
gcaggaacat	gtggagtagt	gatgggtctga	aagaagttgg	aaagaggaac	1200
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agtgaagtgt	tgacttgaaa	cttcaggcag	attaaaagaa	tcatttggtg	1300
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caataagcaa	atgcaaaaaat	attcaatag			1379

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<210> 410
<211> 360
<212> PRT
<213> Homo sapiens
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<400> 410

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20 25 30

Arg Gly Val Glu Val Ala Glu Glu Ser Gly Arg Leu Trp Ser Glu
35 40 45

Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly
50 55 60

Glu Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala
65 70 75

Glu Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His

80										85					90				
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val					
				95					100					105					
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu					
				110					115					120					
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly					
				125					130					135					
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu					
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Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn					
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Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg					
				170					175					180					
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met					
				185					190					195					
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys					
				200					205					210					
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser					
				215					220					225					
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu					
				230					235					240					
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr					
				245					250					255					
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly					
				260					265					270					
Ala	Lys	Pro	Met	Ala	Arg	Phe	Asn	His	Thr	Asp	Arg	Thr	Leu	Glu					
				275					280					285					
Thr	Leu	Lys	Ile	Phe	Ile	Phe	Asn	Gln	Thr	Gly	Ile	Glu	Ala	Lys					
				290					295					300					
Lys	Asn	Val	Val	Val	Thr	Gln	Ala	Asp	Gln	Ile	Gly	Pro	Leu	Pro					
				305					310					315					
Ser	Thr	Leu	Ile	Lys	Ser	Val	Asp	Trp	Leu	Leu	Val	Phe	Ser	Leu					
				320					325					330					
Phe	Phe	Leu	Ile	Ser	Phe	Ile	Met	Tyr	Ala	Thr	Ile	Arg	Thr	Glu					
				335					340					345					
Ser	Ile	Arg	Trp	Leu	Ile	Pro	Gly	Gln	Glu	Gln	Glu	His	Val	Glu					
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<210> 411
 <211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 412
<211> 25
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 412
ccacatgttc ctgctcttgt cctgg 25

<210> 413
<211> 45
<212> DNA
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<220>
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<400> 413
cggtagtgac tgtactctag tcctgtttta caccocgtgg tgccg 45

<210> 414
<211> 1196
<212> DNA
<213> Homo sapiens

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ggctcggcgc gcgggctctt cctctttggc cagcccgaact tctcctacaa 150
gcgcagcaat tgcaagccca tcccgggtcaa cctgcagctg tgccacggca 200
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caggtgaagg accgctgcgc cccggtcatg tccgccttcg gcttcccctg 450
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tccccctcgc tagcagcgac cacctcctgc cagccaccga ggaagctcca 550

Trp	Pro	Asp	Met	Leu	Glu	Cys	Asp	Arg	Phe	Pro	Gln	Asp	Asn	Asp	
				140					145					150	
Leu	Cys	Ile	Pro	Leu	Ala	Ser	Ser	Asp	His	Leu	Leu	Pro	Ala	Thr	
				155					160					165	
Glu	Glu	Ala	Pro	Lys	Val	Cys	Glu	Ala	Cys	Lys	Asn	Lys	Asn	Asp	
				170					175					180	
Asp	Asp	Asn	Asp	Ile	Met	Glu	Thr	Leu	Cys	Lys	Asn	Asp	Phe	Ala	
				185					190					195	
Leu	Lys	Ile	Lys	Val	Lys	Glu	Ile	Thr	Tyr	Ile	Asn	Arg	Asp	Thr	
				200					205					210	
Lys	Ile	Ile	Leu	Glu	Thr	Lys	Ser	Lys	Thr	Ile	Tyr	Lys	Leu	Asn	
				215					220					225	
Gly	Val	Ser	Glu	Arg	Asp	Leu	Lys	Lys	Ser	Val	Leu	Trp	Leu	Lys	
				230					235					240	
Asp	Ser	Leu	Gln	Cys	Thr	Cys	Glu	Glu	Met	Asn	Asp	Ile	Asn	Ala	
				245					250					255	
Pro	Tyr	Leu	Val	Met	Gly	Gln	Lys	Gln	Gly	Gly	Glu	Leu	Val	Ile	
				260					265					270	
Thr	Ser	Val	Lys	Arg	Trp	Gln	Lys	Gly	Gln	Arg	Glu	Phe	Lys	Arg	
				275					280					285	
Ile	Ser	Arg	Ser	Ile	Arg	Lys	Leu	Gln	Cys						
				290					295						

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 416
 cctggctcgc tgctgctgct c 21

<210> 417
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 417
 cctcacaggt gcactgcaag ctgtc 25

<210> 418
 <211> 47
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

ctcttctctt ttggccagcc cgacttctcc tacaagcgca gaattgc 47

<210> 419

<211> 1830

<212> DNA

<213> Homo sapiens

<400> 419

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cgctgggtgt tctgtctgc gatcagcctg ctcaactgct ccaacgccac 150
gctgtggctc agctttgcac ctgtggctga cgtcattgct gaggacttgg 200
tctgtccat ggagcagatc aactggctgt cactggtcta cctcgtggta 250
tcaccccat ttggcgtggc ggccatctgg atcctggact ccgtcgggct 300
ccgtgcggcg accatcctgg gtgcgtggct gaactttgcc gggagtgtgc 350
tacgcatggg gccctgcatg gttgttggga cccaaaaccc atttgccttc 400
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ctctccagcc aagctggctg ccttgtgggt cccagagcac cagcagacca 500
cggccaacat gctcgccacc atgtcgaacc ctctgggcgt ccttgtggcc 550
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tggagttggc ggtcagagtgt tccttccccg tgggggaggg ggctgccaca 1150
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<210> 420

<211> 560

<212> PRT

<213> Homo sapiens

<400> 420

Met	Ala	Gly	Pro	Thr	Glu	Ala	Glu	Thr	Gly	Leu	Ala	Glu	Pro	Arg
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Ala	Leu	Cys	Ala	Gln	Arg	Gly	His	Arg	Thr	Tyr	Ala	Arg	Arg	Trp
				20					25					30

Val	Phe	Leu	Leu	Ala	Ile	Ser	Leu	Leu	Asn	Cys	Ser	Asn	Ala	Thr
				35					40					45

Leu	Trp	Leu	Ser	Phe	Ala	Pro	Val	Ala	Asp	Val	Ile	Ala	Glu	Asp
				50					55					60

Leu	Val	Leu	Ser	Met	Glu	Gln	Ile	Asn	Trp	Leu	Ser	Leu	Val	Tyr
				65					70					75

Leu	Val	Val	Ser	Thr	Pro	Phe	Gly	Val	Ala	Ala	Ile	Trp	Ile	Leu
				80					85					90

Asp	Ser	Val	Gly	Leu	Arg	Ala	Ala	Thr	Ile	Leu	Gly	Ala	Trp	Leu
				95					100					105

Asn	Phe	Ala	Gly	Ser	Val	Leu	Arg	Met	Val	Pro	Cys	Met	Val	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Gly Thr Gln Asn	Pro Phe Ala Phe Leu	Met Gly Gly Gln Ser Leu	110	115	120
	125	130			135
Cys Ala Leu Ala	Gln Ser Leu Val Ile	Phe Ser Pro Ala Lys Leu	140	145	150
Ala Ala Leu Trp	Phe Pro Glu His Gln	Arg Ala Thr Ala Asn Met	155	160	165
Leu Ala Thr Met	Ser Asn Pro Leu Gly	Val Leu Val Ala Asn Val	170	175	180
Leu Ser Pro Val	Leu Val Lys Lys Gly	Glu Asp Ile Pro Leu Met	185	190	195
Leu Gly Val Tyr	Thr Ile Pro Ala Gly	Val Val Cys Leu Leu Ser	200	205	210
Thr Ile Cys Leu	Trp Glu Ser Val Pro	Pro Thr Pro Pro Ser Ala	215	220	225
Gly Ala Ala Ser	Ser Thr Ser Glu Lys	Phe Leu Asp Gly Leu Lys	230	235	240
Leu Gln Leu Met	Trp Asn Lys Ala Tyr	Val Ile Leu Ala Val Cys	245	250	255
Leu Gly Gly Met	Ile Gly Ile Ser Ala	Ser Phe Ser Ala Leu Leu	260	265	270
Glu Gln Ile Leu	Cys Ala Ser Gly His	Ser Ser Gly Phe Ser Gly	275	280	285
Leu Cys Gly Ala	Leu Phe Ile Thr Phe	Gly Ile Leu Gly Ala Leu	290	295	300
Ala Leu Gly Pro	Tyr Val Asp Arg Thr	Lys His Phe Thr Glu Ala	305	310	315
Thr Lys Ile Gly	Leu Cys Leu Phe Ser	Leu Ala Cys Val Pro Phe	320	325	330
Ala Leu Val Ser	Gln Leu Gln Gly Gln	Thr Leu Ala Leu Ala Ala	335	340	345
Thr Cys Ser Leu	Leu Gly Leu Phe Gly	Phe Ser Val Gly Pro Val	350	355	360
Ala Met Glu Leu	Ala Val Glu Cys Ser	Phe Pro Val Gly Glu Gly	365	370	375
Ala Ala Thr Gly	Met Ile Phe Val Leu	Gly Gln Ala Glu Gly Ile	380	385	390
Leu Ile Met Leu	Ala Met Thr Ala Leu	Thr Val Arg Arg Ser Glu	395	400	405

Pro	Ser	Leu	Ser	Thr	Cys	Gln	Gln	Gly	Glu	Asp	Pro	Leu	Asp	Trp
				410					415					420
Thr	Val	Ser	Leu	Leu	Leu	Met	Ala	Gly	Leu	Cys	Thr	Phe	Phe	Ser
				425					430					435
Cys	Ile	Leu	Ala	Val	Phe	Phe	His	Thr	Pro	Tyr	Arg	Arg	Leu	Gln
				440					445					450
Ala	Glu	Ser	Gly	Glu	Pro	Pro	Ser	Thr	Arg	Asn	Ala	Val	Gly	Gly
				455					460					465
Ala	Asp	Ser	Gly	Pro	Gly	Val	Asp	Arg	Gly	Gly	Ala	Gly	Arg	Ala
				470					475					480
Gly	Val	Leu	Gly	Pro	Ser	Thr	Ala	Thr	Pro	Glu	Cys	Thr	Ala	Arg
				485					490					495
Gly	Ala	Ser	Leu	Glu	Asp	Pro	Arg	Gly	Pro	Gly	Ser	Pro	His	Pro
				500					505					510
Ala	Cys	His	Arg	Ala	Thr	Pro	Arg	Ala	Gln	Gly	Pro	Ala	Ala	Thr
				515					520					525
Asp	Ala	Pro	Ser	Arg	Pro	Gly	Arg	Leu	Ala	Gly	Arg	Val	Gln	Ala
				530					535					540
Ser	Arg	Phe	Ile	Asp	Pro	Ala	Gly	Ser	His	Ser	Ser	Phe	Ser	Ser
				545					550					555
Pro	Trp	Val	Ile	Thr										
				560										

<210> 421

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

agcttctcag ccctcctgga gcag 24

<210> 422

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 422

cggttcaata aacctggacg cttgg 25

<210> 423

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 423

tatgtggacc ggaccaagca cttcactgag gccaccaaga ttg 43

<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

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tggccttgcc ttggggtcct gcttgtttca taatcatcta actatgggac 200
aaggttgtgc cggcagctct gggggaagga gcacggggct gatcaagcca 250
tccaggaaac actggaggac ttgtccagcc ttgaaagaac tctagtggtt 300
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 aaaaaaaaaa aaa 4313

<210> 425
 <211> 1184
 <212> PRT
 <213> Homo sapiens

<400> 425

Met	Met	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Gly	Leu	Leu	Gly	Pro	Gly	1	5	10	15
Gly	Tyr	Leu	Phe	Leu	Leu	Gly	Asp	Cys	Gln	Glu	Val	Thr	Thr	Leu	20	25	30	
Thr	Val	Lys	Tyr	Gln	Val	Ser	Glu	Glu	Val	Pro	Ser	Gly	Thr	Val	35	40	45	
Ile	Gly	Lys	Leu	Ser	Gln	Glu	Leu	Gly	Arg	Glu	Glu	Arg	Arg	Arg	50	55	60	
Gln	Ala	Gly	Ala	Ala	Phe	Gln	Val	Leu	Gln	Leu	Pro	Gln	Ala	Leu	65	70	75	
Pro	Ile	Gln	Val	Asp	Ser	Glu	Glu	Gly	Leu	Leu	Ser	Thr	Gly	Arg	80	85	90	
Arg	Leu	Asp	Arg	Glu	Gln	Leu	Cys	Arg	Gln	Trp	Asp	Pro	Cys	Leu	95	100	105	
Val	Ser	Phe	Asp	Val	Leu	Ala	Thr	Gly	Asp	Leu	Ala	Leu	Ile	His	110	115	120	
Val	Glu	Ile	Gln	Val	Leu	Asp	Ile	Asn	Asp	His	Gln	Pro	Arg	Phe	125	130	135	
Pro	Lys	Gly	Glu	Gln	Glu	Leu	Glu	Ile	Ser	Glu	Ser	Ala	Ser	Leu	140	145	150	
Arg	Thr	Arg	Ile	Pro	Leu	Asp	Arg	Ala	Leu	Asp	Pro	Asp	Thr	Gly	155	160	165	
Pro	Asn	Thr	Leu	His	Thr	Tyr	Thr	Leu	Ser	Pro	Ser	Glu	His	Phe	170	175	180	
Ala	Leu	Asp	Val	Ile	Val	Gly	Pro	Asp	Glu	Thr	Lys	His	Ala	Glu	185	190	195	

Leu Ile Val Val	Lys Glu Leu Asp Arg	Glu Ile His Ser Phe Phe	200	205	210
Asp Leu Val Leu	Thr Ala Tyr Asp Asn	Gly Asn Pro Pro Lys Ser	215	220	225
Gly Thr Ser Leu	Val Lys Val Asn Val	Leu Asp Ser Asn Asp Asn	230	235	240
Ser Pro Ala Phe	Ala Glu Ser Ser Leu	Ala Leu Glu Ile Gln Glu	245	250	255
Asp Ala Ala Pro	Gly Thr Leu Leu Ile	Lys Leu Thr Ala Thr Asp	260	265	270
Pro Asp Gln Gly	Pro Asn Gly Glu Val	Glu Phe Phe Leu Ser Lys	275	280	285
His Met Pro Pro	Glu Val Leu Asp Thr	Phe Ser Ile Asp Ala Lys	290	295	300
Thr Gly Gln Val	Ile Leu Arg Arg Pro	Leu Asp Tyr Glu Lys Asn	305	310	315
Pro Ala Tyr Glu	Val Asp Val Gln Ala	Arg Asp Leu Gly Pro Asn	320	325	330
Pro Ile Pro Ala	His Cys Lys Val Leu	Ile Lys Val Leu Asp Val	335	340	345
Asn Asp Asn Ile	Pro Ser Ile His Val	Thr Trp Ala Ser Gln Pro	350	355	360
Ser Leu Val Ser	Glu Ala Leu Pro Lys	Asp Ser Phe Ile Ala Leu	365	370	375
Val Met Ala Asp	Asp Leu Asp Ser Gly	His Asn Gly Leu Val His	380	385	390
Cys Trp Leu Ser	Gln Glu Leu Gly His	Phe Arg Leu Lys Arg Thr	395	400	405
Asn Gly Asn Thr	Tyr Met Leu Leu Thr	Asn Ala Thr Leu Asp Arg	410	415	420
Glu Gln Trp Pro	Lys Tyr Thr Leu Thr	Leu Leu Ala Gln Asp Gln	425	430	435
Gly Leu Gln Pro	Leu Ser Ala Lys Lys	Gln Leu Ser Ile Gln Ile	440	445	450
Ser Asp Ile Asn	Asp Asn Ala Pro Val	Phe Glu Lys Ser Arg Tyr	455	460	465
Glu Val Ser Thr	Arg Glu Asn Asn Leu	Pro Ser Leu His Leu Ile	470	475	480
Thr Ile Lys Ala	His Asp Ala Asp Leu	Gly Ile Asn Gly Lys Val			

Leu Arg Gly Gln Ala Gly Glu Pro Cys Glu Val Gly Gln Ser His	785	790	795
Lys Asp Val Asp Lys Glu Ala Met Met Glu Ala Gly Trp Asp Pro	800	805	810
Cys Leu Gln Ala Pro Phe His Leu Thr Pro Thr Leu Tyr Arg Thr	815	820	825
Leu Arg Asn Gln Gly Asn Gln Gly Ala Pro Ala Glu Ser Arg Glu	830	835	840
Val Leu Gln Asp Thr Val Asn Leu Leu Phe Asn His Pro Arg Gln	845	850	855
Arg Asn Ala Ser Arg Glu Asn Leu Asn Leu Pro Glu Pro Gln Pro	860	865	870
Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser	875	880	885
Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro	890	895	900
Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His	905	910	915
Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln	920	925	930
Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu	935	940	945
Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln	950	955	960
Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln	965	970	975
Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly	980	985	990
Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg	995	1000	1005
Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp	1010	1015	1020
Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu	1025	1030	1035
Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu	1040	1045	1050
Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu	1055	1060	1065
Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala			

1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala		
1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val		
1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser		
1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser		
1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala		
1145	1150	1155
Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr		
1160	1165	1170
Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Ser Arg Cys Leu		
1175	1180	

<210> 426

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 426

gtaagcacat gcctccagag gtgc 24

<210> 427

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 427

gtgacgtgga tgcttgggat gttg 24

<210> 428

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 428

tggacacctt cagtattgat gccaaagacag gccaggatcat tctgcgtcga 50

<210> 429

<211> 2037

<212> DNA

<213> Homo sapiens

<400> 429

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ggcctcgggg agtgggaagt ggaggcagga gccttcctta cacttcgcca 150
tgagtttcct catcgactcc agcatcatga ttacctcca gatactat 200
tttggatttg ggtggctttt ctcatgcgc caattgttta aagactatga 250
gatacgtcag tatgttgtag aggtgatctt ctccgtgacg tttgcatttt 300
cttgacccat gtttgagctc atcatctttg aaatcttagg agtattgaat 350
agcagctccc gttattttca ctggaaaatg aacctgtgtg taattctgct 400
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ctgaccttta tgtatttctt ctggaaacta ggagatccct tccccattct 550
cagcccaaaa catgggatct tatccataga acagctcatc agccgggttg 600
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 tttgccttga gattgactca ttaaaatcag agactgtaac aaaaaaaaaa 1950
 aaaaaaaaaa agggcgccgc cgactctaga gtcgacctgc agaagcttgg 2000
 ccgccatggc ccaacttggtt tattgcagct tataatg 2037

<210> 430
 <211> 455
 <212> PRT
 <213> Homo sapiens

<400> 430
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 1 5 10 15
 Leu Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe
 20 25 30
 Lys Asp Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser
 35 40 45
 Val Thr Phe Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe
 50 55 60
 Glu Ile Leu Gly Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp
 65 70 75
 Lys Met Asn Leu Cys Val Ile Leu Leu Ile Leu Val Phe Met Val
 80 85 90
 Pro Phe Tyr Ile Gly Tyr Phe Ile Val Ser Asn Ile Arg Leu Leu
 95 100 105
 His Lys Gln Arg Leu Leu Phe Ser Cys Leu Leu Trp Leu Thr Phe
 110 115 120

Met Tyr Phe Phe Trp Lys Leu Gly Asp	Pro Phe Pro Ile Leu Ser	125	130	135
Pro Lys His Gly Ile Leu Ser Ile Glu Gln Leu Ile Ser Arg Val		140	145	150
Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu Ser Gly Phe Gly		155	160	165
Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe Leu Arg Asn		170	175	180
Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu Leu Gln		185	190	195
Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met Ala		200	205	210
Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser		215	220	225
Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly		230	235	240
Ser Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu		245	250	255
Glu Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala		260	265	270
Thr Lys Glu Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr		275	280	285
Phe Asn Phe Leu Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys		290	295	300
Ile Phe Met Ala Thr Ile Asn Ile Val Phe Asp Arg Val Gly Lys		305	310	315
Thr Asp Pro Val Thr Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu		320	325	330
Gly Ile Gln Phe Asp Val Lys Phe Trp Ser Gln His Ile Ser Phe		335	340	345
Ile Leu Val Gly Ile Ile Ile Val Thr Ser Ile Arg Gly Leu Leu		350	355	360
Ile Thr Leu Thr Lys Phe Phe Tyr Ala Ile Ser Ser Ser Lys Ser		365	370	375
Ser Asn Val Ile Val Leu Leu Leu Ala Gln Ile Met Gly Met Tyr		380	385	390
Phe Val Ser Ser Val Leu Leu Ile Arg Met Ser Met Pro Leu Glu		395	400	405
Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu Gln Phe Asn				

410	415	420
Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser Ala Leu		
425	430	435
Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro Glu		
440	445	450
Lys Gln Met Ala Pro		
455		

<210> 431
 <211> 407
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 78, 81, 113, 157, 224, 297
 <223> unknown base

<400> 431
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 tcgactccag catcatgatt acctcccnga nactatTTTT tggatttggg 100
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 ttgtacnggt gatcttctcc gtgacgtttg ccatttcttg caccatgttt 200
 gagctcatca tctttgaaat cttnngagta ttgaatagca gctcccgta 250
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 tgggtgccttt ttacattggc tattttattg tgagcaatat ccgactactg 350
 cataaacaac gactgctttt ttctgtctc ttatggctga cctttatgta 400
 tttccag 407

<210> 432
 <211> 457
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434
 <223> unknown base

<400> 432
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 tatttttttg atttggggta gntttttttc atgcgccaat tgtttaaaga 150
 ctatgagata cgtcagtatg ttgtacaggt gatnttntcc gtgacgtttg 200

cattttcttg caccatgttt gagctcatca tntttgaaat nttaggagta 250
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 tgagcaatat ccgactactg cataaacaac gactgctttt ttcctgtctn 400
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 cattctc 457

<210> 433
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 433
 aagtggagcc ggagccttcc 20

<210> 434
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 434
 tcgttggtta tgcagtagtc gg 22

<210> 435
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 435
 attgtttaaa gactatgaga tacgtcagta tgttgtacag g 41

<210> 436
 <211> 3951
 <212> DNA
 <213> Homo sapiens

<400> 436
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a 3951

<210> 437

<211> 1141

<212> PRT

<213> Homo sapiens

<400> 437

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Cys	Tyr	Leu	Phe	Gly	Ser	Leu	Leu	Val	Glu	Leu	Leu	Phe	Ser	Arg
				20					25					30

Ala	Val	Ala	Phe	Asn	Leu	Asp	Val	Met	Gly	Ala	Leu	Arg	Lys	Glu
				35					40					45

Gly	Glu	Pro	Gly	Ser	Leu	Phe	Gly	Phe	Ser	Val	Ala	Leu	His	Arg
				50					55					60

Gln	Leu	Gln	Pro	Arg	Pro	Gln	Ser	Trp	Leu	Leu	Val	Gly	Ala	Pro
				65					70					75

Gln	Ala	Leu	Ala	Leu	Pro	Gly	Gln	Gln	Ala	Asn	Arg	Thr	Gly	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

80

85

90

Leu Phe Ala Cys Pro Leu Ser Leu Glu Glu Thr Asp Cys Tyr Arg
95 100 105

Val Asp Ile Asp Gln Gly Ala Asp Met Gln Lys Glu Ser Lys Glu
110 115 120

Asn Gln Trp Leu Gly Val Ser Val Arg Ser Gln Gly Pro Gly Gly
125 130 135

Lys Ile Val Thr Cys Ala His Arg Tyr Glu Ala Arg Gln Arg Val
140 145 150

Asp Gln Ile Leu Glu Thr Arg Asp Met Ile Gly Arg Cys Phe Val
155 160 165

Leu Ser Gln Asp Leu Ala Ile Arg Asp Glu Leu Asp Gly Gly Glu
170 175 180

Trp Lys Phe Cys Glu Gly Arg Pro Gln Gly His Glu Gln Phe Gly
185 190 195

Phe Cys Gln Gln Gly Thr Ala Ala Ala Phe Ser Pro Asp Ser His
200 205 210

Tyr Leu Leu Phe Gly Ala Pro Gly Thr Tyr Asn Trp Lys Gly Thr
215 220 225

Ala Arg Val Glu Leu Cys Ala Gln Gly Ser Ala Asp Leu Ala His
230 235 240

Leu Asp Asp Gly Pro Tyr Glu Ala Gly Gly Glu Lys Glu Gln Asp
245 250 255

Pro Arg Leu Ile Pro Val Pro Ala Asn Ser Tyr Phe Gly Phe Ser
260 265 270

Ile Asp Ser Gly Lys Gly Leu Val Arg Ala Glu Glu Leu Ser Phe
275 280 285

Val Ala Gly Ala Pro Arg Ala Asn His Lys Gly Ala Val Val Ile
290 295 300

Leu Arg Lys Asp Ser Ala Ser Arg Leu Val Pro Glu Val Met Leu
305 310 315

Ser Gly Glu Arg Leu Thr Ser Gly Phe Gly Tyr Ser Leu Ala Val
320 325 330

Ala Asp Leu Asn Ser Asp Gly Trp Pro Asp Leu Ile Val Gly Ala
335 340 345

Pro Tyr Phe Phe Glu Arg Gln Glu Glu Leu Gly Gly Ala Val Tyr
350 355 360

Val Tyr Leu Asn Gln Gly Gly His Trp Ala Gly Ile Ser Pro Leu
365 370 375

302

Arg	Leu	Cys	Gly	Ser	Pro	Asp	Ser	Met	Phe	Gly	Ile	Ser	Leu	Ala		380	385	390
Val	Leu	Gly	Asp	Leu	Asn	Gln	Asp	Gly	Phe	Pro	Asp	Ile	Ala	Val		395	400	405
Gly	Ala	Pro	Phe	Asp	Gly	Asp	Gly	Lys	Val	Phe	Ile	Tyr	His	Gly		410	415	420
Ser	Ser	Leu	Gly	Val	Val	Ala	Lys	Pro	Ser	Gln	Val	Leu	Glu	Gly		425	430	435
Glu	Ala	Val	Gly	Ile	Lys	Ser	Phe	Gly	Tyr	Ser	Leu	Ser	Gly	Ser		440	445	450
Leu	Asp	Met	Asp	Gly	Asn	Gln	Tyr	Pro	Asp	Leu	Leu	Val	Gly	Ser		455	460	465
Leu	Ala	Asp	Thr	Ala	Val	Leu	Phe	Arg	Ala	Arg	Pro	Ile	Leu	His		470	475	480
Val	Ser	His	Glu	Val	Ser	Ile	Ala	Pro	Arg	Ser	Ile	Asp	Leu	Glu		485	490	495
Gln	Pro	Asn	Cys	Ala	Gly	Gly	His	Ser	Val	Cys	Val	Asp	Leu	Arg		500	505	510
Val	Cys	Phe	Ser	Tyr	Ile	Ala	Val	Pro	Ser	Ser	Tyr	Ser	Pro	Thr		515	520	525
Val	Ala	Leu	Asp	Tyr	Val	Leu	Asp	Ala	Asp	Thr	Asp	Arg	Arg	Leu		530	535	540
Arg	Gly	Gln	Val	Pro	Arg	Val	Thr	Phe	Leu	Ser	Arg	Asn	Leu	Glu		545	550	555
Glu	Pro	Lys	His	Gln	Ala	Ser	Gly	Thr	Val	Trp	Leu	Lys	His	Gln		560	565	570
His	Asp	Arg	Val	Cys	Gly	Asp	Ala	Met	Phe	Gln	Leu	Gln	Glu	Asn		575	580	585
Val	Lys	Asp	Lys	Leu	Arg	Ala	Ile	Val	Val	Thr	Leu	Ser	Tyr	Ser		590	595	600
Leu	Gln	Thr	Pro	Arg	Leu	Arg	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu		605	610	615
Pro	Pro	Val	Ala	Pro	Ile	Leu	Asn	Ala	His	Gln	Pro	Ser	Thr	Gln		620	625	630
Arg	Ala	Glu	Ile	His	Phe	Leu	Lys	Gln	Gly	Cys	Gly	Glu	Asp	Lys		635	640	645
Ile	Cys	Gln	Ser	Asn	Leu	Gln	Leu	Val	His	Ala	Arg	Phe	Cys	Thr		650	655	660
Arg	Val	Ser	Asp	Thr	Glu	Phe	Gln	Pro	Leu	Pro	Met	Asp	Val	Asp				

665										670					675				
Gly	Thr	Thr	Ala	Leu	Phe	Ala	Leu	Ser	Gly	Gln	Pro	Val	Ile	Gly					
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Leu	Glu	Leu	Met	Val	Thr	Asn	Leu	Pro	Ser	Asp	Pro	Ala	Gln	Pro					
				695					700					705					
Gln	Ala	Asp	Gly	Asp	Asp	Ala	His	Glu	Ala	Gln	Leu	Leu	Val	Met					
				710					715					720					
Leu	Pro	Asp	Ser	Leu	His	Tyr	Ser	Gly	Val	Arg	Ala	Leu	Asp	Pro					
				725					730					735					
Ala	Glu	Lys	Pro	Leu	Cys	Leu	Ser	Asn	Glu	Asn	Ala	Ser	His	Val					
				740					745					750					
Glu	Cys	Glu	Leu	Gly	Asn	Pro	Met	Lys	Arg	Gly	Ala	Gln	Val	Thr					
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Phe	Tyr	Leu	Ile	Leu	Ser	Thr	Ser	Gly	Ile	Ser	Ile	Glu	Thr	Thr					
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Glu	Leu	Glu	Val	Glu	Leu	Leu	Leu	Ala	Thr	Ile	Ser	Glu	Gln	Glu					
				785					790					795					
Leu	His	Pro	Val	Ser	Ala	Arg	Ala	Arg	Val	Phe	Ile	Glu	Leu	Pro					
				800					805					810					
Leu	Ser	Ile	Ala	Gly	Met	Ala	Ile	Pro	Gln	Gln	Leu	Phe	Phe	Ser					
				815					820					825					
Gly	Val	Val	Arg	Gly	Glu	Arg	Ala	Met	Gln	Ser	Glu	Arg	Asp	Val					
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Ser	Leu	Arg	Thr	Leu	Gly	Ser	Ala	Phe	Leu	Asn	Ile	Met	Trp	Pro					
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Glu	Leu	Glu	Gly	Gly	Gln	Gly	Pro	Gly	Gln	Lys	Gly	Leu	Cys	Ser					
				890					895					900					
Pro	Arg	Pro	Asn	Ile	Leu	His	Leu	Asp	Val	Asp	Ser	Arg	Asp	Arg					
				905					910					915					
Arg	Arg	Arg	Glu	Leu	Glu	Pro	Pro	Glu	Gln	Gln	Glu	Pro	Gly	Glu					
				920					925					930					
Arg	Gln	Glu	Pro	Ser	Met	Ser	Trp	Trp	Pro	Val	Ser	Ser	Ala	Glu					
				935					940					945					
Lys	Lys	Lys	Asn	Ile	Thr	Leu	Asp	Cys	Ala	Arg	Gly	Thr	Ala	Asn					
				950					955					960					

Cys	Val	Val	Phe	Ser	Cys	Pro	Leu	Tyr	Ser	Phe	Asp	Arg	Ala	Ala	
				965					970					975	
Val	Leu	His	Val	Trp	Gly	Arg	Leu	Trp	Asn	Ser	Thr	Phe	Leu	Glu	
				980					985					990	
Glu	Tyr	Ser	Ala	Val	Lys	Ser	Leu	Glu	Val	Ile	Val	Arg	Ala	Asn	
				995					1000					1005	
Ile	Thr	Val	Lys	Ser	Ser	Ile	Lys	Asn	Leu	Met	Leu	Arg	Asp	Ala	
				1010					1015					1020	
Ser	Thr	Val	Ile	Pro	Val	Met	Val	Tyr	Leu	Asp	Pro	Met	Ala	Val	
				1025					1030					1035	
Val	Ala	Glu	Gly	Val	Pro	Trp	Trp	Val	Ile	Leu	Leu	Ala	Val	Leu	
				1040					1045					1050	
Ala	Gly	Leu	Leu	Val	Leu	Ala	Leu	Leu	Val	Leu	Leu	Leu	Trp	Lys	
				1055					1060					1065	
Met	Gly	Phe	Phe	Lys	Arg	Ala	Lys	His	Pro	Glu	Ala	Thr	Val	Pro	
				1070					1075					1080	
Gln	Tyr	His	Ala	Val	Lys	Ile	Pro	Arg	Glu	Asp	Arg	Gln	Gln	Phe	
				1085					1090					1095	
Lys	Glu	Glu	Lys	Thr	Gly	Thr	Ile	Leu	Arg	Asn	Asn	Trp	Gly	Ser	
				1100					1105					1110	
Pro	Arg	Arg	Glu	Gly	Pro	Asp	Ala	His	Pro	Ile	Leu	Ala	Ala	Asp	
				1115					1120					1125	
Gly	His	Pro	Glu	Leu	Gly	Pro	Asp	Gly	His	Pro	Gly	Pro	Gly	Thr	
				1130					1135					1140	

Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

ggctgacacc gcagtgtctt tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439
gctgctgggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

catcctccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

cgcgccgggc gcagggagct gaggggacgg ctcgagacgg cggcgcgtgc 50

agcagctcca gaaagcagcg agttggcaga gcagggctgc atttccagca 100

ggagctgcga gcacagtgtt ggctcacaac aagatgtctc aggtgtcagc 150

cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctgcgagctg 200

ccgcggcggg ggctgcagcc ggggggcggg cggacggcgg taattttctg 250

gatgataaac aatgggtcac cacaatctct cagtatgaca aggaagtcgg 300

acagtggaaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350

ggagtccagg aaaacccttc gatcaggctt tagatccagc taaggatcca 400

tgcttaaaga tgaaatgtag tcgccataaa gtatgcattg ctcaagattc 450

tcagactgca gtctgcatta gtcaccggag gcttacacac aggatgaaag 500

aagcaggagt agaccatagg cagtggaggg gtcccatatt atccacctgc 550

aagcagtgcc cagtgggtcta tcccagccct gtttgtggtt cagatggtca 600

tacctactct tttcagtgc aactagaata tcaggcatgt gtcttaggaa 650

aacagatctc agtcaaagt gaaggacatt gcccatgtcc ttcagataag 700

cccaccagta caagcagaaa tgtaagaga gcatgcagtg acctggagtt 750

caggggaagt gcaaacagat tgccgggactg gttcaaggcc cttcatgaaa 800

gtggaagtca aaacaagaag acaaaaacat tgctgaggcc tgagagaagc 850

agattcgata ccagcatctt gccaatgtgc aaggactcac ttggctggat 900

gtttaacaga cttgatacaa actatgacct gctattggac cagtcagagc 950

Tyr	Tyr	Lys	Pro	Thr	Gln	Cys	His	Gly	Ser	Val	Gly	Gln	Cys	Trp
				350					355					360
Cys	Val	Asp	Arg	Tyr	Gly	Asn	Glu	Val	Met	Gly	Ser	Arg	Ile	Asn
				365					370					375
Gly	Val	Ala	Asp	Cys	Ala	Ile	Asp	Phe	Glu	Ile	Ser	Gly	Asp	Phe
				380					385					390
Ala	Ser	Gly	Asp	Phe	His	Glu	Trp	Thr	Asp	Asp	Glu	Asp	Asp	Glu
				395					400					405
Asp	Asp	Ile	Met	Asn	Asp	Glu	Asp	Glu	Ile	Glu	Asp	Asp	Asp	Glu
				410					415					420
Asp	Glu	Gly	Asp	Asp	Asp	Asp	Gly	Gly	Asp	Asp	His	Asp	Val	Tyr
				425					430					435

Ile

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<210> 443
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 443
cagcaatatt cagaagcggc aaggg 25

<210> 444
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 444
catcatggtc atcaccacca tcatcatc 28

<210> 445
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 445
ggttactaca agccaacaca atgtcatggc agtggttgac agtgctgg 48

<210> 446
<211> 3617
<212> DNA
<213> Homo sapiens

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<400> 446

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gagcggagac aacagtacct gacgcctctt tcagcccggg atcgccccag 100
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gctctgcctc cgggtgctgct gcctggggcg gccggcttca caccttccct 200
cgatagcgac ttcaccttta cccttcccgc cggccagaag gagtgtttct 250
accagcccat gccctgaag gcctcgctgg agatcgagta ccaagtttta 300
gatggagcag gattagatat tgatttccat cttgcctctc cagaaggcaa 350
aaccttagtt tttgaacaaa gaaaatcaga tggagtccac actgtagaga 400
ctgaagtgg tgattacatg ttctgctttg acaatacatt cagcaccatt 450
tctgagaagg tgattttctt tgaattaatc ctggataata tgggagaaca 500
ggcacaagaa caagaagatt ggaagaaata tattactggc acagatatat 550
tggatatgaa actggaagac atcctggaat ccatcaacag catcaagtcc 600
agactaagca aaagtgggca catacaaatt ctgcttagag catttgaagc 650
tcgtgatcga aacatacaag aaagcaactt tgatagagtc aatttctggt 700
ctatggttaa tttagtggtc atggtggtgg tgtcagccat tcaagtttat 750
atgctgaaga gtctgtttga agataagagg aaaagtagaa cttaaaactc 800
caaactagag tacgtaacat tgaaaaatga ggcataaaaa tgcaataaac 850
tgttacagtc aagaccatta atggtcttct ccaaaatatt ttgagatata 900
aaagtaggaa acaggtataa ttttaatgtg aaaattaagt cttcactttc 950
tgtgcaagta atcctgctga tccagttgta ctttaagtgtg taacaggaat 1000
attttgcaga atataggttt aactgaatga agccatatta ataactgcat 1050
tttctaact ttgaaaaatt ttgcaaatgt cttaggtgat ttaaataaat 1100
gagtattggg cctaattgca acaccagtct gtttttaaca ggttctatta 1150
cccagaactt ttttgtaa at gcggcagtta caaattaact gtggaagttt 1200
tcagttttaa gttataaatc acctgagaat tacctaataa tggattgaat 1250
aatcttttag actacaaaag cccaactttt ctctattttac atatgcatct 1300
ctcctataat gtaaataagaa taatagcttt gaaatacaat taggtttttg 1350
agatttttat aaccaaatac atttcagtgt aacatattag cagaaagcat 1400
tagtctttgt actttgctta cattcccaaa agctgacatt ttcacgattc 1450

taccatataa aaacgataat tgctttatctt ggaaaagaat ttaggaatac 2950
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 cataaccaa aaagcaaaac ttgtaaacag agtaaaaatc tttaatatctt 3050
 ctaaagacat actgtttatc tgcttcatat gcttttttta atttcactat 3100
 tccatttcta aattaaagtt atgctaaatt gagtaagctg tttatcactt 3150
 aacagctcat tttgtctttt tcaatataca aatttttaaaa atactacaat 3200
 atttaactaa ggcccaaccg atttcataa tgtagcagtt accgtgttca 3250
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 gtacaataat gcacaatcag tggtgctcaa actgctttat acttataaac 3550
 agccattctta aataagcaac gtattgtgag tactgatatg tatataataa 3600
 aaattatcaa aggaaaa 3617

<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

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Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30
Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45
Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60
Glu	Tyr	Gln	Val	Leu	Asp	Gly	Ala	Gly	Leu	Asp	Ile	Asp	Phe	His
				65					70					75
Leu	Ala	Ser	Pro	Glu	Gly	Lys	Thr	Leu	Val	Phe	Glu	Gln	Arg	Lys
				80					85					90
Ser	Asp	Gly	Val	His	Thr	Val	Glu	Thr	Glu	Val	Gly	Asp	Tyr	Met
				95					100					105
Phe	Cys	Phe	Asp	Asn	Thr	Phe	Ser	Thr	Ile	Ser	Glu	Lys	Val	Ile

	110		115		120
Phe Phe Glu Leu	Ile Leu Asp Asn Met	Gly Glu Gln Ala Gln	Glu		
	125		130		135
Gln Glu Asp Trp	Lys Lys Tyr Ile Thr	Gly Thr Asp Ile Leu	Asp		
	140		145		150
Met Lys Leu Glu	Asp Ile Leu Glu Ser	Ile Asn Ser Ile Lys	Ser		
	155		160		165
Arg Leu Ser Lys	Ser Gly His Ile Gln	Ile Leu Leu Arg Ala	Phe		
	170		175		180
Glu Ala Arg Asp	Arg Asn Ile Gln Glu	Ser Asn Phe Asp Arg	Val		
	185		190		195
Asn Phe Trp Ser	Met Val Asn Leu Val	Val Met Val Val Val	Ser		
	200		205		210
Ala Ile Gln Val	Tyr Met Leu Lys Ser	Leu Phe Glu Asp Lys	Arg		
	215		220		225

Lys Ser Arg Thr

<210> 448

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 448

cccagcaggg ctgggcgaca aga 23

<210> 449

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 449

gtcttccagt ttcatatcca ata 23

<210> 450

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

ccagaaggag cacggggaag ggcagccaga tcttgtcgcc cat 43

<210> 451
 <211> 859
 <212> DNA
 <213> Homo sapiens

<400> 451
 ccatccctga gatcttttta taaaaaaccc agtccttgct gaccagacaa 50
 agcataccag atctcaccag agagtcgcag acactatgct gcctcccatg 100
 gccctgcca gtgtgtcctg gatgctgctt tcttgctca ttctcctgtg 150
 tcagggtcaa ggtgaagaaa ccagaagga actgccctct ccacggatca 200
 gctgtcccaa aggtccaag gcctatggct cccctgcta tgccttggtt 250
 ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300
 ctctggaaaa ctggtgtctg tgctcagtgg ggctgagggg tccttcgtgt 350
 cctccctggt gaggagcatt agtaacagct actcatacat ctggattggg 400
 ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450
 gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500
 ccatcttaaa ccctggccac tgtgggagcc tgtcaagaag cacaggattt 550
 ctgaagtgga aagattataa ctgtgatgca aagttaccct atgtctgcaa 600
 gttcaaggac tagggcaggt ggaagtcag cagcctcagc ttggcgtgca 650
 gctcatcatg gacatgagac cagtgtgaag actcaccctg gaagagaata 700
 ttctcccaa actgccctac ctgactacct tgatcatgac ctcttctttt 750
 ttctttttt ttaccttca ttccaggctt ttctctgtct tccatgtctt 800
 gagatctcag agaataataa taaaatggt actttataaa aaaaaaaaaa 850
 aaaaaaaaaa 859

<210> 452
 <211> 175
 <212> PRT
 <213> Homo sapiens

<400> 452
 Met Leu Pro Pro Met Ala Leu Pro Ser Val Ser Trp Met Leu Leu
 1 5 10 15
 Ser Cys Leu Ile Leu Leu Cys Gln Val Gln Gly Glu Glu Thr Gln
 20 25 30
 Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys
 35 40 45
 Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser

	50	55	60
Trp Met Asp Ala Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly Lys	65	70	75
Leu Val Ser Val Leu Ser Gly Ala Glu Gly Ser Phe Val Ser Ser	80	85	90
Leu Val Arg Ser Ile Ser Asn Ser Tyr Ser Tyr Ile Trp Ile Gly	95	100	105
Leu His Asp Pro Thr Gln Gly Ser Glu Pro Asp Gly Asp Gly Trp	110	115	120
Glu Trp Ser Ser Thr Asp Val Met Asn Tyr Phe Ala Trp Glu Lys	125	130	135
Asn Pro Ser Thr Ile Leu Asn Pro Gly His Cys Gly Ser Leu Ser	140	145	150
Arg Ser Thr Gly Phe Leu Lys Trp Lys Asp Tyr Asn Cys Asp Ala	155	160	165
Lys Leu Pro Tyr Val Cys Lys Phe Lys Asp	170	175	

<210> 453

<211> 550

<212> DNA

<213> Homo sapiens

<400> 453

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ccagtctgtc gccacctcac ttggtgtctg ctgtccccgc caggcaagcc 50
tggggtgaga gcacagagga gtgggccggg accatgcggg ggacgcggct 100
ggcgctcctg gcgctggtgc tggctgcctg cggagagctg gcgccggccc 150
tgcgctgcta cgtctgtccg gagcccacag gagtgtcgga ctgtgtcacc 200
atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250
ccgggagata gtgtaccctt tccaggggga ctccacggtg accaagtcct 300
gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350
cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgcccgc 400
tctgaacagc ctccactgcg gggccctcac gctcctccca ctcttgagcc 450
tccgactgta gagtccccgc ccacccccat ggccctatgc ggcccagccc 500
cgaatgcctt gaagaagtgc cccctgcacc agggaaaaaa aaaaaaaaaa 550

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<210> 454

<211> 125

<212> PRT

<213> Homo sapiens

<400> 454

Met Arg Gly Thr Arg Leu Ala Leu Leu Ala Leu Val Leu Ala Ala
1 5 10 15

Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu
20 25 30

Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr
35 40 45

Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val
50 55 60

Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser
65 70 75

Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro
80 85 90

Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro
95 100 105

Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu
110 115 120

Leu Ser Leu Arg Leu
125

<210> 455

<211> 1518

<212> DNA

<213> Homo sapiens

<400> 455

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gcgcagcggg agctacccgg gtctttgtcg cgatggtagc ggcggtcttc 200

ggcgccacc ctctgctggg agtgagcgcc accttgaact cggttctcaa 250

ttccaacgct atcaagaacc tgccccacc gctggggcggc gctgcggggc 300

accaggctc tgagtcagc gccgcgccg gaatcctgta cccgggcggg 350

aataagtacc agaccattga caactaccag ccgtaccgt gcgcagagga 400

cgaggagtgc ggcactgatg agtactgcgc tagtcccacc cgcggagggg 450

acgcaggcgt gcaaattctgt ctgcctgca ggaagcgccg aaaacgctgc 500

atgcgtcacg ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550

tgtgtcttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600

ctgaaagctt tggtaatgat catagcacct tggatgggta ttccagaaga 650
 accaccttgt cttcaaaaat gtatcacacc aaaggacaag aaggttctgt 700
 ttgtctccgg tcatcagact gtgcctcagg attgtgttgt gctagacact 750
 tctgggtccaa gatctgtaaa cctgtcctga aagaagggtca agtgtgtacc 800
 aagcatagga gaaaaggctc tcatggacta gaaatattcc agcgttggtta 850
 ctgtggagaa ggtctgtctt gccggataca gaaagatcac catcaagcca 900
 gtaattcttc taggcttcac acttgtcaga gacactaaac cagctatcca 950
 aatgcagtga actcctttta tataatagat gctatgaaaa ccttttatga 1000
 ccttcatcaa ctcaatccta aggatataca agttctgtgg tttcagttaa 1050
 gcattccaat aacaccttcc aaaaacctgg agtgtaagag ctttgtttct 1100
 ttatggaact cccctgtgat tgcagtaa at tactgtattg taaattctca 1150
 gtgtggcact tacctgtaaa tgcaatgaaa cttttaatta tttttctaaa 1200
 ggtgctgcac tgcctathtt tcctcttgtt atgtaaatht ttgtacacat 1250
 tgattgttat cttgactgac aaatattcta tattgaactg aagtaaataca 1300
 tttcagctta tagttcttaa aagcataacc ctttaccoca ttttaattcta 1350
 gagtctagaa cgcaaggatc tcttggaatg acaaatagata ggtacctaaa 1400
 atgtaacatg aaaatactag cttattttct gaaatgtact atcttaatgc 1450
 ttaaattata tttcccttta ggctgtgata gtttttgaaa taaaatttaa 1500
 catttaaaaa aaaaaaaaa 1518

<210> 456

<211> 266

<212> PRT

<213> Homo sapiens

<400> 456

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Met	Val	Ala	Ala	Ala	Leu	Gly	Gly	His	Pro	Leu	Leu	Gly	Val	Ser
				20					25					30
Ala	Thr	Leu	Asn	Ser	Val	Leu	Asn	Ser	Asn	Ala	Ile	Lys	Asn	Leu
				35					40					45
Pro	Pro	Pro	Leu	Gly	Gly	Ala	Ala	Gly	His	Pro	Gly	Ser	Ala	Val
				50					55					60
Ser	Ala	Ala	Pro	Gly	Ile	Leu	Tyr	Pro	Gly	Gly	Asn	Lys	Tyr	Gln
				65					70					75

Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu	
				80					85					90	
Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp	
				95					100					105	
Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg	
				110					115					120	
Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn	
				125					130					135	
Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile	
				140					145					150	
Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu	
				155					160					165	
Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His	
				170					175					180	
Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys	
				185					190					195	
Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys	
				200					205					210	
Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg	
				215					220					225	
Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly	
				230					235					240	
Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser	
				245					250					255	
Asn	Ser	Ser	Arg	Leu	His	Thr	Cys	Gln	Arg	His					
				260					265						

<210> 457
 <211> 638
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> unsure
 <222> 30, 123, 133, 139, 180, 214, 259, 282, 308, 452, 467, 471, 473, 509, 556
 <223> unknown base

 <400> 457
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 catttttttt tctttctcct tcnngagtcc ttntgagang atggtttttg 150
 gcgcagcggg agctaacccg gttttttgtn gcgatggtag cggcgggtttt 200

cggcggccac cttntgctgg gagtgagcgc caccttgaat cggttttcaa 250
 ttccaacgnt atcaagaacc tgccccacc gntgggcggc gctgcggggc 300
 acccaggntt tgcagtcagc gccgcgccg gaatcctgta cccgggcggg 350
 aataagtacc agaccattga caattaccag ccgtaccgt gcgcagagga 400
 cgaggagtgc ggcaactgat agtactgcgc tagtcccacc cgcgaggagg 450
 angcgggcgt gcaaanttgt ntngcctgca ggaagcgccg aaaacgctgc 500
 atgcgtcang ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550
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<211> 4040

<212> DNA

<213> Homo sapiens

<400> 458

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<211> 747

<212> PRT

<213> Homo sapiens

<400> 459

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				20					25					30
Gly	Thr	Asp	Gln	Asp	Phe	Tyr	Ser	Leu	Leu	Gly	Val	Ser	Lys	Thr
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Ala	Ser	Ser	Arg	Glu	Ile	Arg	Gln	Ala	Phe	Lys	Lys	Leu	Ala	Leu
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Lys	Leu	His	Pro	Asp	Lys	Asn	Pro	Asn	Asn	Pro	Asn	Ala	His	Gly
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Asp	Phe	Gly	Ile	Tyr	Asp	Asp	Asp	Pro	Glu	Ile	Ile	Thr	Leu	Glu
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Arg	Arg	Glu	Phe	Asp	Ala	Ala	Val	Asn	Ser	Gly	Glu	Leu	Trp	Phe
				140					145					150
Val	Asn	Phe	Tyr	Ser	Pro	Gly	Cys	Ser	His	Cys	His	Asp	Leu	Ala
				155					160					165
Pro	Thr	Trp	Arg	Asp	Phe	Ala	Lys	Glu	Val	Asp	Gly	Leu	Leu	Arg
				170					175					180
Ile	Gly	Ala	Val	Asn	Cys	Gly	Asp	Asp	Arg	Met	Leu	Cys	Arg	Met
				185					190					195
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<210> 461

<211> 24

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 461

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<210> 462

<211> 50

<212> DNA

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<400> 462

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<210> 463

<211> 1818

<212> DNA

<213> Homo sapiens

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<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

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35 40 45

Gly Pro Pro Leu Pro Thr Pro Gly Pro Asp Arg Asp Arg Glu Leu
50 55 60

Thr Ala Asp Ser Asp Val Asp Glu Phe Leu Asp Lys Phe Leu Ser
65 70 75

Ala Gly Val Lys Gln Ser Asp Leu Pro Arg Lys Glu Thr Glu Gln
80 85 90

Pro Pro Ala Pro Gly Ser Met Glu Glu Ser Val Arg Gly Tyr Asp
95 100 105

Trp Ser Pro Arg Asp Ala Arg Arg Ser Pro Asp Gln Gly Arg Gln
110 115 120

Gln Ala Glu Arg Arg Ser Val Leu Arg Gly Phe Cys Ala Asn Ser
125 130 135

Ser Leu Ala Phe Pro Thr Lys Glu Arg Ala Phe Asp Asp Ile Pro
140 145 150

Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp Arg His Gly Ala
155 160 165

Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn Trp Lys Arg
170 175 180

Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly Ala Pro
185 190 195

Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn Ala
200 205 210

Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys
215 220 225

Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys
230 235 240

Phe	Leu	Phe	Val	Arg	Asp	Pro	Phe	Val	Arg	Leu	Ile	Ser	Ala	Phe	
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Arg	Ser	Lys	Phe	Glu	Leu	Glu	Asn	Glu	Glu	Phe	Tyr	Arg	Lys	Phe	
				260					265					270	
Ala	Val	Pro	Met	Leu	Arg	Leu	Tyr	Ala	Asn	His	Thr	Ser	Leu	Pro	
				275					280					285	
Ala	Ser	Ala	Arg	Glu	Ala	Phe	Arg	Ala	Gly	Leu	Lys	Val	Ser	Phe	
				290					295					300	
Ala	Asn	Phe	Ile	Gln	Tyr	Leu	Leu	Asp	Pro	His	Thr	Glu	Lys	Leu	
				305					310					315	
Ala	Pro	Phe	Asn	Glu	His	Trp	Arg	Gln	Val	Tyr	Arg	Leu	Cys	His	
				320					325					330	
Pro	Cys	Gln	Ile	Asp	Tyr	Asp	Phe	Val	Gly	Lys	Leu	Glu	Thr	Leu	
				335					340					345	
Asp	Glu	Asp	Ala	Ala	Gln	Leu	Leu	Gln	Leu	Leu	Gln	Val	Asp	Arg	
				350					355					360	
Gln	Leu	Arg	Phe	Pro	Pro	Ser	Tyr	Arg	Asn	Arg	Thr	Ala	Ser	Ser	
				365					370					375	
Trp	Glu	Glu	Asp	Trp	Phe	Ala	Lys	Ile	Pro	Leu	Ala	Trp	Arg	Gln	
				380					385					390	
Gln	Leu	Tyr	Lys	Leu	Tyr	Glu	Ala	Asp	Phe	Val	Leu	Phe	Gly	Tyr	
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Pro	Lys	Pro	Glu	Asn	Leu	Leu	Arg	Asp							
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 <212> DNA
 <213> Homo sapiens

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<211> 270

<212> PRT

<213> Homo sapiens

<400> 468

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				20					25					30

Asn	Ser	Gly	Ala	Arg	Val	Val	Ile	Cys	Asp	Lys	Asp	Glu	Ser	Gly
				35					40					45

Gly	Arg	Ala	Leu	Glu	Gln	Glu	Leu	Pro	Gly	Ala	Val	Phe	Ile	Leu
				50					55					60

Cys	Asp	Val	Thr	Gln	Glu	Asp	Asp	Val	Lys	Thr	Leu	Val	Ser	Glu
				65					70					75

Thr	Ile	Arg	Arg	Phe	Gly	Arg	Leu	Asp	Cys	Val	Val	Asn	Asn	Ala
				80					85					90

Gly	His	His	Pro	Pro	Pro	Gln	Arg	Pro	Glu	Glu	Thr	Ser	Ala	Gln
				95					100					105

Gly	Phe	Arg	Gln	Leu	Leu	Glu	Leu	Asn	Leu	Leu	Gly	Thr	Tyr	Thr
				110					115					120

Leu	Thr	Lys	Leu	Ala	Leu	Pro	Tyr	Leu	Arg	Lys	Ser	Gln	Gly	Asn	
				125					130					135	
Val	Ile	Asn	Ile	Ser	Ser	Leu	Val	Gly	Ala	Ile	Gly	Gln	Ala	Gln	
				140					145					150	
Ala	Val	Pro	Tyr	Val	Ala	Thr	Lys	Gly	Ala	Val	Thr	Ala	Met	Thr	
				155					160					165	
Lys	Ala	Leu	Ala	Leu	Asp	Glu	Ser	Pro	Tyr	Gly	Val	Arg	Val	Asn	
				170					175					180	
Cys	Ile	Ser	Pro	Gly	Asn	Ile	Trp	Thr	Pro	Leu	Trp	Glu	Glu	Leu	
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Ala	Ala	Leu	Met	Pro	Asp	Pro	Arg	Ala	Thr	Ile	Arg	Glu	Gly	Met	
				200					205					210	
Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly	
				215					220					225	
Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly	
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Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys	
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<211> 687

<212> DNA

<213> Homo sapiens

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<211> 180
<212> PRT
<213> Homo sapiens

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35 40 45
Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu
50 55 60
Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn
65 70 75
Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu
80 85 90
Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile
95 100 105
Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg
110 115 120
Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp
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Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg
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<210> 472

<211> 349

<212> PRT

<213> Homo sapiens

<400> 472

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			20					25						30
Ala	Leu	Pro	Pro	Glu	Gln	Ser	Arg	Val	Gln	Pro	Met	Thr	Ala	Ser
			35					40						45
Asn	Trp	Thr	Leu	Val	Met	Glu	Gly	Glu	Trp	Met	Leu	Lys	Phe	Tyr
			50					55						60
Ala	Pro	Trp	Cys	Pro	Ser	Cys	Gln	Gln	Thr	Asp	Ser	Glu	Trp	Glu
			65					70						75
Ala	Phe	Ala	Lys	Asn	Gly	Glu	Ile	Leu	Gln	Ile	Ser	Val	Gly	Lys
			80					85						90

Val	Asp	Val	Ile	Gln	Glu	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Phe	Val	95	100	105
Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg	110	115	120
Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile	125	130	135
Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys	140	145	150
Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser	155	160	165
Ile	Ser	Gly	Lys	Ile	Trp	His	Leu	His	Asn	Tyr	Phe	Thr	Val	Thr	170	175	180
Leu	Gly	Ile	Pro	Ala	Trp	Cys	Ser	Tyr	Val	Phe	Phe	Val	Ile	Ala	185	190	195
Thr	Leu	Val	Phe	Gly	Leu	Phe	Met	Gly	Leu	Val	Leu	Val	Val	Ile	200	205	210
Ser	Glu	Cys	Phe	Tyr	Val	Pro	Leu	Pro	Arg	His	Leu	Ser	Glu	Arg	215	220	225
Ser	Glu	Gln	Asn	Arg	Arg	Ser	Glu	Glu	Ala	His	Arg	Ala	Glu	Gln	230	235	240
Leu	Gln	Asp	Ala	Glu	Glu	Glu	Lys	Asp	Asp	Ser	Asn	Glu	Glu	Glu	245	250	255
Asn	Lys	Asp	Ser	Leu	Val	Asp	Asp	Glu	Glu	Glu	Lys	Glu	Asp	Leu	260	265	270
Gly	Asp	Glu	Asp	Glu	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Asn	Leu	275	280	285
Ala	Ala	Gly	Val	Asp	Glu	Glu	Arg	Ser	Glu	Ala	Asn	Asp	Gln	Gly	290	295	300
Pro	Pro	Gly	Glu	Asp	Gly	Val	Thr	Arg	Glu	Glu	Val	Glu	Pro	Glu	305	310	315
Glu	Ala	Glu	Glu	Gly	Ile	Ser	Glu	Gln	Pro	Cys	Pro	Ala	Asp	Thr	320	325	330
Glu	Val	Val	Glu	Asp	Ser	Leu	Arg	Gln	Arg	Lys	Ser	Gln	His	Ala	335	340	345
Asp Lys Gly Leu																	

<210> 473

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 474
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<212> DNA
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<223> Synthetic oligonucleotide probe

<400> 474
ctctcctcat ccacaccagc agcc 24

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<220>
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<210> 476
<211> 2478
<212> DNA
<213> Homo sapiens

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tcaagaacaa tggaatatca tcctgattta gaaaatttgg atgaagatgg 200
atatactcaa ttacacttcg actctcaaag caataccagg atagctgttg 250
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<210> 477

<211> 201

<212> PRT

<213> Homo sapiens

<400> 477

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Val	Ser	Glu	Lys	Gly	Ser	Cys	Ala	Ala	Ser	Pro	Pro	Trp	Arg	Leu	35	40	45	
Ile	Ala	Val	Ile	Leu	Gly	Ile	Leu	Cys	Leu	Val	Ile	Leu	Val	Ile	50	55	60	
Ala	Val	Val	Leu	Gly	Thr	Met	Gly	Val	Leu	Ser	Ser	Pro	Cys	Pro	65	70	75	
Pro	Asn	Trp	Ile	Ile	Tyr	Glu	Lys	Ser	Cys	Tyr	Leu	Phe	Ser	Met	80	85	90	
Ser	Leu	Asn	Ser	Trp	Asp	Gly	Ser	Lys	Arg	Gln	Cys	Trp	Gln	Leu	95	100	105	
Gly	Ser	Asn	Leu	Leu	Lys	Ile	Asp	Ser	Ser	Asn	Glu	Leu	Gly	Phe	110	115	120	
Ile	Val	Lys	Gln	Val	Ser	Ser	Gln	Pro	Asp	Asn	Ser	Phe	Trp	Ile	125	130	135	
Gly	Leu	Ser	Arg	Pro	Gln	Thr	Glu	Val	Pro	Trp	Leu	Trp	Glu	Asp	140	145	150	
Gly	Ser	Thr	Phe	Ser	Ser	Asn	Leu	Phe	Gln	Ile	Arg	Thr	Thr	Ala	155	160	165	
Thr	Gln	Glu	Asn	Pro	Ser	Pro	Asn	Cys	Val	Trp	Ile	His	Val	Ser				

170

175

180

Val Ile Tyr Asp Gln Leu Cys Ser Val Pro Ser Tyr Ser Ile Cys
185 190 195

Glu Lys Lys Phe Ser Met
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<210> 478

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 478

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<210> 479

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 479

acaagtgtct tcccaacctg 20

<210> 480

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 480

atcctcccag agccatggta cctc 24

<210> 481

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 481

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<210> 482

<211> 3819

<212> DNA

<213> Homo sapiens

<400> 482

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<211> 693

<212> PRT

<213> Homo sapiens

<400> 483

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			20						25					30
Asp	Phe	Arg	Phe	Cys	Ser	Gln	Arg	Asn	Gln	Thr	His	Arg	Ser	Ser
			35						40					45
Leu	His	Tyr	Lys	Pro	Thr	Pro	Asp	Leu	Arg	Ile	Ser	Ile	Glu	Asn
			50						55					60
Ser	Glu	Glu	Ala	Leu	Thr	Val	His	Ala	Pro	Phe	Pro	Ala	Ala	His
			65						70					75

Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Tyr	His	Phe	80	85	90
Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	95	100	105
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	110	115	120
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	125	130	135
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	140	145	150
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	155	160	165
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	170	175	180
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	185	190	195
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	200	205	210
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	215	220	225
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	230	235	240
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	245	250	255
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	260	265	270
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Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	290	295	300
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Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	320	325	330
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	335	340	345
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	350	355	360
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr			

Ser Cys Phe Cys	Asn His Leu Thr Tyr	Phe Ala Val Leu Met Val	365	370	375
	380	385			390
Ser Ser Val Glu	Val Asp Ala Val His	Lys His Tyr Leu Ser Leu	395	400	405
Leu Ser Tyr Val	Gly Cys Val Val Ser	Ala Leu Ala Cys Leu Val	410	415	420
Thr Ile Ala Ala	Tyr Leu Cys Ser Arg	Val Pro Leu Pro Cys Arg	425	430	435
Arg Lys Pro Arg	Asp Tyr Thr Ile Lys	Val His Met Asn Leu Leu	440	445	450
Leu Ala Val Phe	Leu Leu Asp Thr Ser	Phe Leu Leu Ser Glu Pro	455	460	465
Val Ala Leu Thr	Gly Ser Glu Ala Gly	Cys Arg Ala Ser Ala Ile	470	475	480
Phe Leu His Phe	Ser Leu Leu Thr Cys	Leu Ser Trp Met Gly Leu	485	490	495
Glu Gly Tyr Asn	Leu Tyr Arg Leu Val	Val Glu Val Phe Gly Thr	500	505	510
Tyr Val Pro Gly	Tyr Leu Leu Lys Leu	Ser Ala Met Gly Trp Gly	515	520	525
Phe Pro Ile Phe	Leu Val Thr Leu Val	Ala Leu Val Asp Val Asp	530	535	540
Asn Tyr Gly Pro	Ile Ile Leu Ala Val	His Arg Thr Pro Glu Gly	545	550	555
Val Ile Tyr Pro	Ser Met Cys Trp Ile	Arg Asp Ser Leu Val Ser	560	565	570
Tyr Ile Thr Asn	Leu Gly Leu Phe Ser	Leu Val Phe Leu Phe Asn	575	580	585
Met Ala Met Leu	Ala Thr Met Val Val	Gln Ile Leu Arg Leu Arg	590	595	600
Pro His Thr Gln	Lys Trp Ser His Val	Leu Thr Leu Leu Gly Leu	605	610	615
Ser Leu Val Leu	Gly Leu Pro Trp Ala	Leu Ile Phe Phe Ser Phe	620	625	630
Ala Ser Gly Thr	Phe Gln Leu Val Val	Leu Tyr Leu Phe Ser Ile	635	640	645
Ile Thr Ser Phe	Gln Gly Phe Leu Ile	Phe Ile Trp Tyr Trp Ser	650	655	660

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn
665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser
680 685 690

Ser Arg Ile

<210> 484
<211> 516
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 68, 70, 84, 147
<223> unknown base

<400> 484
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cggtgccct gacaggctct gaaggctggc tgccgagcca gtgccatctt 200
cctgcacttc tcctgctcac ctgcctttcc tggatggggc tcgaggggta 250
caacctctac cgactcgtgg tggaggcttt tggcaacctat gtccctggct 300
acctactcaa gctgagcgcc atgggctggg gcttcccat ctttctggtg 350
acgctggtgg ccctggtgga tgtggacaac tatggcccca tcattcttggc 400
tgtgcatagg actccagagg gcgtcatcta cccttccatg tgctggatcc 450
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tttctgttca acatgg 516

<210> 485
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 485
ggcattggag cagtgctggg tg 22

<210> 486
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 486
tggaggccta gatgcggctg gacg 24

<210> 487
<211> 2849
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 2715
<223> unknown base

<400> 487
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ggttcaggtc cagggtttgc tttgatcctt ttcaaaaact ggagacacag 100
aagaggggctc taggaaaaag ttttgatgg gattatgtgg aaactaccct 150
gcgattctct gctgccagag caggctcggc gcttccaccc cagtgcagcc 200
ttcccctggc ggtggtgaaa gagactcggg agtcgctgct tccaaagtgc 250
ccgccgtgag tgagctctca cccagtcag ccaaatgagc ctcttcgggc 300
ttctcctgct gacatctgcc ctggccggcc agagacaggg gactcaggcg 350
gaatccaacc tgagtagtaa attccagttt tccagcaaca aggaacagaa 400
cggagtacaa gatcctcagc atgagagaat tattactgtg tctactaatg 450
gaagtattca cagcccaagg tttcctcata cttatccaag aaatacggtc 500
ttggtatgga gattagtagc agtagaggaa aatgtatgga tacaacttac 550
gtttgatgaa agatttgggc ttgaagacc agaagatgac atatgcaagt 600
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tggtgtggtt ctggtactgt accaggaaaa cagatttcta aaggaaatca 700
aattaggata agatttgtat ctgatgaata ttttccttct gaaccagggt 750
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cttggaagg cttttgtttt tggaagaaaa tccagagtgg tggatctgaa 1000
ccttctaaca gaggaggtaa gattatacag ctgcacacct cgtaacttct 1050

cagtgtccat aagggaagaa ctaaagagaa ccgataccat tttctggcca 1100
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 acgaggtcct tcagttgaga ccaaagaccg gtgtcagggg attgcacaaa 1250
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 ccatccttaa tctcagttgt ttgcttcaag gacctttcat cttcaggatt 1450
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 atgtaaacca gaacattcta tgtaactaaa acctgggttt taaaaaggaa 1850
 ctatgttgct atgaattaaa cttgtgtcat gctgatagga cagactggat 1900
 ttttcatatt tcttattaaa atttctgcca tttagaagaa gagaactaca 1950
 ttcattggtt ggaagagata aacctgaaaa gaagagtggc cttatcttca 2000
 ctttatcgat aagtcagttt atttggttca ttgtgtacat ttttatattc 2050
 tccttttgac attataactg ttggcttttc taatcttggt aaatatatct 2100
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 tggaatagaa ttggtaaagt gcaaagactt tttgaaaata attaaattat 2350
 catatcttcc attcctgtta ttggagatga aaataaaaag caacttatga 2400
 aagtagacat tcagatccag ccattactaa cctattcctt ttttggggaa 2450
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gcttcctgat aaagcgtgct gtgctgtgca gtaggaacac atcctattta 2550
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 aaaatgctta atatngtgcc taggttatgt ggtgactatt tgaatcaaaa 2750
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 aaaaaaaaaa aaaaaaaaaa aggttttaggg ataacagggt aatgcggcc 2849

<210> 488
 <211> 345
 <212> PRT
 <213> Homo sapiens

<400> 488

Met	Ser	Leu	Phe	Gly	Leu	Leu	Leu	Leu	Thr	Ser	Ala	Leu	Ala	Gly	1	5	10	15
Gln	Arg	Gln	Gly	Thr	Gln	Ala	Glu	Ser	Asn	Leu	Ser	Ser	Lys	Phe	20	25	30	
Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln	35	40	45	
His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser	50	55	60	
Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp	65	70	75	
Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe	80	85	90	
Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys	95	100	105	
Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu	110	115	120	
Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser	125	130	135	
Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe	140	145	150	
Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met	Pro	155	160	165	
Gln	Phe	Thr	Glu	Ala	Val	Ser	Pro	Ser	Val	Leu	Pro	Pro	Ser	Ala	170	175	180	
Leu	Pro	Leu	Asp	Leu	Leu	Asn	Asn	Ala	Ile	Thr	Ala	Phe	Ser	Thr	185	190	195	

Leu	Glu	Asp	Leu	Ile	Arg	Tyr	Leu	Glu	Pro	Glu	Arg	Trp	Gln	Leu	
				200					205					210	
Asp	Leu	Glu	Asp	Leu	Tyr	Arg	Pro	Thr	Trp	Gln	Leu	Leu	Gly	Lys	
				215					220					225	
Ala	Phe	Val	Phe	Gly	Arg	Lys	Ser	Arg	Val	Val	Asp	Leu	Asn	Leu	
				230					235					240	
Leu	Thr	Glu	Glu	Val	Arg	Leu	Tyr	Ser	Cys	Thr	Pro	Arg	Asn	Phe	
				245					250					255	
Ser	Val	Ser	Ile	Arg	Glu	Glu	Leu	Lys	Arg	Thr	Asp	Thr	Ile	Phe	
				260					265					270	
Trp	Pro	Gly	Cys	Leu	Leu	Val	Lys	Arg	Cys	Gly	Gly	Asn	Cys	Ala	
				275					280					285	
Cys	Cys	Leu	His	Asn	Cys	Asn	Glu	Cys	Gln	Cys	Val	Pro	Ser	Lys	
				290					295					300	
Val	Thr	Lys	Lys	Tyr	His	Glu	Val	Leu	Gln	Leu	Arg	Pro	Lys	Thr	
				305					310					315	
Gly	Val	Arg	Gly	Leu	His	Lys	Ser	Leu	Thr	Asp	Val	Ala	Leu	Glu	
				320					325					330	
His	His	Glu	Glu	Cys	Asp	Cys	Val	Cys	Arg	Gly	Ser	Thr	Gly	Gly	
				335					340					345	

<210> 489

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 489

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<210> 490

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 490

gaactaaaga gaaccgatac cattttctgg ccaggttgtc 40

<210> 491

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 491

caccacagcg tttaaccagg 20

<210> 492

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 492

acaacaggca cagttcccac 20

<210> 493

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 493

ggcggaatcc aacctgagta g 21

<210> 494

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 494

gcggctatcc tcctgtgctc 20

<210> 495

<211> 3283

<212> DNA

<213> Homo sapiens

<400> 495

cccatctcaa gctgatcttg gcacctctca tgctctgctc tttcaacca 50

gacctctaca ttccattttg gaagaagact aaaaatgggtg tttccaatgt 100

ggacactgaa gagacaaatt cttatccttt ttaacataat cctaatttcc 150

aaactccttg gggctagatg gtttcctaaa actctgccct gtgatgtcac 200

tctggatggt ccaaagaacc atgtgatcgt ggactgcaca gacaagcatt 250

tgacagaaat tcctggaggt attcccacga acaccacgaa cctcacctc 300

accattaacc acataaccaga catctcccca gcgtcctttc acagactgga 350

ccatctggta gagatcgatt tcagatgcaa ctgtgtacct attccactgg 400
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<210> 496

<211> 1049

<212> PRT

<213> Homo sapiens

<400> 496

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Phe	Asn	Ile	Ile	Leu	Ile	Ser	Lys	Leu	Leu	Gly	Ala	Arg	Trp	Phe
				20					25					30

Pro	Lys	Thr	Leu	Pro	Cys	Asp	Val	Thr	Leu	Asp	Val	Pro	Lys	Asn
				35					40					45

His	Val	Ile	Val	Asp	Cys	Thr	Asp	Lys	His	Leu	Thr	Glu	Ile	Pro
				50					55					60

Gly	Gly	Ile	Pro	Thr	Asn	Thr	Thr	Asn	Leu	Thr	Leu	Thr	Ile	Asn
				65					70					75

His	Ile	Pro	Asp	Ile	Ser	Pro	Ala	Ser	Phe	His	Arg	Leu	Asp	His
				80					85					90

Leu	Val	Glu	Ile	Asp	Phe	Arg	Cys	Asn	Cys	Val	Pro	Ile	Pro	Leu
				95					100					105

Gly	Ser	Lys	Asn	Asn	Met	Cys	Ile	Lys	Arg	Leu	Gln	Ile	Lys	Pro
				110					115					120

Arg	Ser	Phe	Ser	Gly	Leu	Thr	Tyr	Leu	Lys	Ser	Leu	Tyr	Leu	Asp
				125					130					135

Gly	Asn	Gln	Leu	Leu	Glu	Ile	Pro	Gln	Gly	Leu	Pro	Pro	Ser	Leu
				140					145					150

Gln	Leu	Leu	Ser	Leu	Glu	Ala	Asn	Asn	Ile	Phe	Ser	Ile	Arg	Lys
				155					160					165

Glu	Asn	Leu	Thr	Glu	Leu	Ala	Asn	Ile	Glu	Ile	Leu	Tyr	Leu	Gly
				170					175					180

Gln	Asn	Cys	Tyr	Tyr	Arg	Asn	Pro	Cys	Tyr	Val	Ser	Tyr	Ser	Ile
				185					190					195

Glu	Lys	Asp	Ala	Phe	Leu	Asn	Leu	Thr	Lys	Leu	Lys	Val	Leu	Ser
				200					205					210

Leu	Lys	Asp	Asn	Asn	Val	Thr	Ala	Val	Pro	Thr	Val	Leu	Pro	Ser
				215					220					225

Thr	Leu	Thr	Glu	Leu	Tyr	Leu	Tyr	Asn	Asn	Met	Ile	Ala	Lys	Ile
				230					235					240

Gln	Glu	Asp	Asp	Phe	Asn	Asn	Leu	Asn	Gln	Leu	Gln	Ile	Leu	Asp
				245					250					255

Leu	Ser	Gly	Asn	Cys	Pro	Arg	Cys	Tyr	Asn	Ala	Pro	Phe	Pro	Cys	
				260					265					270	
Ala	Pro	Cys	Lys	Asn	Asn	Ser	Pro	Leu	Gln	Ile	Pro	Val	Asn	Ala	
				275					280					285	
Phe	Asp	Ala	Leu	Thr	Glu	Leu	Lys	Val	Leu	Arg	Leu	His	Ser	Asn	
				290					295					300	
Ser	Leu	Gln	His	Val	Pro	Pro	Arg	Trp	Phe	Lys	Asn	Ile	Asn	Lys	
				305					310					315	
Leu	Gln	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Phe	Leu	Ala	Lys	Glu	Ile	
				320					325					330	
Gly	Asp	Ala	Lys	Phe	Leu	His	Phe	Leu	Pro	Ser	Leu	Ile	Gln	Leu	
				335					340					345	
Asp	Leu	Ser	Phe	Asn	Phe	Glu	Leu	Gln	Val	Tyr	Arg	Ala	Ser	Met	
				350					355					360	
Asn	Leu	Ser	Gln	Ala	Phe	Ser	Ser	Leu	Lys	Ser	Leu	Lys	Ile	Leu	
				365					370					375	
Arg	Ile	Arg	Gly	Tyr	Val	Phe	Lys	Glu	Leu	Lys	Ser	Phe	Asn	Leu	
				380					385					390	
Ser	Pro	Leu	His	Asn	Leu	Gln	Asn	Leu	Glu	Val	Leu	Asp	Leu	Gly	
				395					400					405	
Thr	Asn	Phe	Ile	Lys	Ile	Ala	Asn	Leu	Ser	Met	Phe	Lys	Gln	Phe	
				410					415					420	
Lys	Arg	Leu	Lys	Val	Ile	Asp	Leu	Ser	Val	Asn	Lys	Ile	Ser	Pro	
				425					430					435	
Ser	Gly	Asp	Ser	Ser	Glu	Val	Gly	Phe	Cys	Ser	Asn	Ala	Arg	Thr	
				440					445					450	
Ser	Val	Glu	Ser	Tyr	Glu	Pro	Gln	Val	Leu	Glu	Gln	Leu	His	Tyr	
				455					460					465	
Phe	Arg	Tyr	Asp	Lys	Tyr	Ala	Arg	Ser	Cys	Arg	Phe	Lys	Asn	Lys	
				470					475					480	
Glu	Ala	Ser	Phe	Met	Ser	Val	Asn	Glu	Ser	Cys	Tyr	Lys	Tyr	Gly	
				485					490					495	
Gln	Thr	Leu	Asp	Leu	Ser	Lys	Asn	Ser	Ile	Phe	Phe	Val	Lys	Ser	
				500					505					510	
Ser	Asp	Phe	Gln	His	Leu	Ser	Phe	Leu	Lys	Cys	Leu	Asn	Leu	Ser	
				515					520					525	
Gly	Asn	Leu	Ile	Ser	Gln	Thr	Leu	Asn	Gly	Ser	Glu	Phe	Gln	Pro	
				530					535					540	
Leu	Ala	Glu	Leu	Arg	Tyr	Leu	Asp	Phe	Ser	Asn	Asn	Arg	Leu	Asp	

545	550	555
Leu Leu His Ser Thr Ala Phe Glu Glu	Leu His Lys Leu Glu Val	
560	565	570
Leu Asp Ile Ser Ser Asn Ser His Tyr	Phe Gln Ser Glu Gly Ile	
575	580	585
Thr His Met Leu Asn Phe Thr Lys Asn	Leu Lys Val Leu Gln Lys	
590	595	600
Leu Met Met Asn Asp Asn Asp Ile Ser	Ser Ser Thr Ser Arg Thr	
605	610	615
Met Glu Ser Glu Ser Leu Arg Thr Leu	Glu Phe Arg Gly Asn His	
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 35 40 45
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Gly	Tyr	Val	Phe	Gln	Glu	Leu	Arg	Glu	Asp	Asp	Phe	Gln	Pro	Leu	380	385	390
Met	Gln	Leu	Pro	Asn	Leu	Ser	Thr	Ile	Asn	Leu	Gly	Ile	Asn	Phe	395	400	405
Ile	Lys	Gln	Ile	Asp	Phe	Lys	Leu	Phe	Gln	Asn	Phe	Ser	Asn	Leu	410	415	420
Glu	Ile	Ile	Tyr	Leu	Ser	Glu	Asn	Arg	Ile	Ser	Pro	Leu	Val	Lys	425	430	435
Asp	Thr	Arg	Gln	Ser	Tyr	Ala	Asn	Ser	Ser	Ser	Phe	Gln	Arg	His	440	445	450
Ile	Arg	Lys	Arg	Arg	Ser	Thr	Asp	Phe	Glu	Phe	Asp	Pro	His	Ser	455	460	465
Asn	Phe	Tyr	His	Phe	Thr	Arg	Pro	Leu	Ile	Lys	Pro	Gln	Cys	Ala	470	475	480
Ala	Tyr	Gly	Lys	Ala	Leu	Asp	Leu	Ser	Leu	Asn	Ser	Ile	Phe	Phe	485	490	495
Ile	Gly	Pro	Asn	Gln	Phe	Glu	Asn	Leu	Pro	Asp	Ile	Ala	Cys	Leu	500	505	510
Asn	Leu	Ser	Ala	Asn	Ser	Asn	Ala	Gln	Val	Leu	Ser	Gly	Thr	Glu	515	520	525
Phe	Ser	Ala	Ile	Pro	His	Val	Lys	Tyr	Leu	Asp	Leu	Thr	Asn	Asn	530	535	540
Arg	Leu	Asp	Phe	Asp	Asn	Ala	Ser	Ala	Leu	Thr	Glu	Leu	Ser	Asp	545	550	555
Leu	Glu	Val	Leu	Asp	Leu	Ser	Tyr	Asn	Ser	His	Tyr	Phe	Arg	Ile	560	565	570
Ala	Gly	Val	Thr	His	His	Leu	Glu	Phe	Ile	Gln	Asn	Phe	Thr	Asn	575	580	585
Leu	Lys	Val	Leu	Asn	Leu	Ser	His	Asn	Asn	Ile	Tyr	Thr	Leu	Thr	590	595	600
Asp	Lys	Tyr	Asn	Leu	Glu	Ser	Lys	Ser	Leu	Val	Glu	Leu	Val	Phe	605	610	615
Ser	Gly	Asn	Arg	Leu	Asp	Ile	Leu	Trp	Asn	Asp	Asp	Asp	Asn	Arg	620	625	630
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650	655	660
Asn Leu Pro Ala Ser Leu Thr Glu Leu	His Ile Asn Asp Asn Met	
665	670	675
Leu Lys Phe Phe Asn Trp Thr Leu Leu	Gln Gln Phe Pro Arg Leu	
680	685	690
Glu Leu Leu Asp Leu Arg Gly Asn Lys	Leu Leu Phe Leu Thr Asp	
695	700	705
Ser Leu Ser Asp Phe Thr Ser Ser Leu	Arg Thr Leu Leu Leu Ser	
710	715	720
His Asn Arg Ile Ser His Leu Pro Ser	Gly Phe Leu Ser Glu Val	
725	730	735
Ser Ser Leu Lys His Leu Asp Leu Ser	Ser Asn Leu Leu Lys Thr	
740	745	750
Ile Asn Lys Ser Ala Leu Glu Thr Lys	Thr Thr Thr Lys Leu Ser	
755	760	765
Met Leu Glu Leu His Gly Asn Pro Phe	Glu Cys Thr Cys Asp Ile	
770	775	780
Gly Asp Phe Arg Arg Trp Met Asp Glu	His Leu Asn Val Lys Ile	
785	790	795
Pro Arg Leu Val Asp Val Ile Cys Ala	Ser Pro Gly Asp Gln Arg	
800	805	810
Gly Lys Ser Ile Val Ser Leu Glu Leu	Thr Thr Cys Val Ser Asp	
815	820	825
Val Thr Ala Val Ile Leu Phe Phe Phe	Thr Phe Phe Ile Thr Thr	
830	835	840
Met Val Met Leu Ala Ala Leu Ala His	His Leu Phe Tyr Trp Asp	
845	850	855
Val Trp Phe Ile Tyr Asn Val Cys Leu	Ala Lys Val Lys Gly Tyr	
860	865	870
Arg Ser Leu Ser Thr Ser Gln Thr Phe	Tyr Asp Ala Tyr Ile Ser	
875	880	885
Tyr Asp Thr Lys Asp Ala Ser Val Thr	Asp Trp Val Ile Asn Glu	
890	895	900
Leu Arg Tyr His Leu Glu Glu Ser Arg	Asp Lys Asn Val Leu Leu	
905	910	915
Cys Leu Glu Glu Arg Asp Trp Asp Pro	Gly Leu Ala Ile Ile Asp	
920	925	930

Asn	Leu	Met	Gln	Ser	Ile	Asn	Gln	Ser	Lys	Lys	Thr	Val	Phe	Val
			935						940					945
Leu	Thr	Lys	Lys	Tyr	Ala	Lys	Ser	Trp	Asn	Phe	Lys	Thr	Ala	Phe
			950						955					960
Tyr	Leu	Ala	Leu	Gln	Arg	Leu	Met	Asp	Glu	Asn	Met	Asp	Val	Ile
			965						970					975
Ile	Phe	Ile	Leu	Leu	Glu	Pro	Val	Leu	Gln	His	Ser	Gln	Tyr	Leu
			980						985					990
Arg	Leu	Arg	Gln	Arg	Ile	Cys	Lys	Ser	Ser	Ile	Leu	Gln	Trp	Pro
			995						1000					1005
Asp	Asn	Pro	Lys	Ala	Glu	Gly	Leu	Phe	Trp	Gln	Thr	Leu	Arg	Asn
			1010						1015					1020
Val	Val	Leu	Thr	Glu	Asn	Asp	Ser	Arg	Tyr	Asn	Asn	Met	Tyr	Val
			1025						1030					1035

Asp Ser Ile Lys Gln Tyr
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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 500

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 500

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<210> 501

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 501

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<210> 502

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<220>
<223> Synthetic oligonucleotide probe

<400> 502
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<210> 503
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 503
catccatgtt ctcattccatt agcc 24

<210> 504
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<210> 505
<211> 1738
<212> DNA
<213> Homo sapiens

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Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val
 20 25 30
 Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val
 35 40 45
 Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg
 50 55 60
 Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg
 65 70 75
 Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro
 80 85 90
 Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala
 95 100 105
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 110 115 120
 Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln
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 Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln
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 155 160 165
 Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly
 170 175 180
 Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala
 185 190 195
 Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu
 200 205 210
 Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala
 215 220 225
 Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu
 230 235 240
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 260 265 270
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 <212> DNA
 <213> Homo sapiens

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gcagcccccga ggaccgggga ggcacagggtg gccccacca cccggaggag 400
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<210> 508

<211> 273

<212> PRT

<213> Homo sapiens

<400> 508

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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val	20	25	30	
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val	35	40	45	
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	50	55	60	
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	65	70	75	
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	80	85	90	
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	95	100	105	
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	110	115	120	
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	125	130	135	
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	140	145	150	
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu	155	160	165	
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	170	175	180	
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	185	190	195	
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	200	205	210	

Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
				215					220					225
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu
				230					235					240
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu
				245					250					255
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys
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Lys Asp Ser

<210> 509
 <211> 1538
 <212> DNA
 <213> Homo sapiens

<400> 509

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<210> 510

<211> 273

<212> PRT

<213> Homo sapiens

<400> 510

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
				50					55					60
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
				65					70					75
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala
				95					100					105
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
				110					115					120
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
				125					130					135
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln

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155	160	165
Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly		
170	175	180
Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala		
185	190	195
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu		
200	205	210
Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala		
215	220	225
Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu		
230	235	240
Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu		
245	250	255
Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys		
260	265	270
Lys Asp Ser		

<210> 511

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 511

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<210> 512

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 512

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<210> 513

<211> 46

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 513

ggtgacactt gccagtcaga tgtggatgaa tgcagtgota ggaggg 46

<210> 514

<211> 2690

<212> DNA

<213> Homo sapiens

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<222> 2039-2065

<223> unknown base

<400> 514

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<210> 515
<211> 364
<212> PRT
<213> Homo sapiens

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35 40 45
Leu Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu
50 55 60
Ala Val Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu
65 70 75
Phe Leu Phe Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp
80 85 90
Pro Gly Val Ile Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile
95 100 105
Glu Met Glu Ile Glu Ala Thr Asn Gly Ala Val Pro Gln Gly Gln
110 115 120
Arg Pro Pro Pro Arg Ile Lys Asn Phe Gln Ile Asn Asn Gln Ile
125 130 135
Val Lys Leu Lys Tyr Cys Tyr Thr Cys Lys Ile Phe Arg Pro Pro
140 145 150
Arg Ala Ser His Cys Ser Ile Cys Asp Asn Cys Val Glu Arg Phe
155 160 165
Asp His His Cys Pro Trp Val Gly Asn Cys Val Gly Lys Arg Asn
170 175 180
Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser Leu Ser Leu Leu Thr
185 190 195
Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val Ala Leu Lys Ser
200 205 210
Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr Pro Gly Thr
215 220 225
Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser Val Val

230	235	240
Gly Leu Thr Gly Phe His Thr Phe Leu Val Ala Leu Asn Gln Thr		
245	250	255
Thr Asn Glu Asp Ile Lys Gly Ser Trp Thr Gly Lys Asn Arg Val		
260	265	270
Gln Asn Pro Tyr Ser His Gly Asn Ile Val Lys Asn Cys Cys Glu		
275	280	285
Val Leu Cys Gly Pro Leu Pro Pro Ser Val Leu Asp Arg Arg Gly		
290	295	300
Ile Leu Pro Leu Glu Glu Ser Gly Ser Arg Pro Pro Ser Thr Gln		
305	310	315
Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu		
320	325	330
His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu		
335	340	345
Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala		
350	355	360
Glu Ala Glu Lys		

<210> 516

<211> 255

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 36, 38, 88, 118, 135, 193, 213, 222

<223> unknown base

<400> 516

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tgaattaggt attataggga tgggtggggtt gatttttntt cctggaggct 100

tttggttttg gactctcnct ttctcccaca gacncttcg accatcactg 150

cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200

tcttcacact ttntctctcc cncctcacia tctatgtcct cgccttcaac 250

atcgt 255

<210> 517

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 517

caacgtgatt tcaaagctgg gctc 24

<210> 518

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 518

gcctcgtatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtggaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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ctcacctgaa atctctcata gccc 24

<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 521

cgcaaaaccc attttgggag caggaattcc aatcatgtct gtgatggtgg 50

<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

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agagcaacac aatctatcag gaaagaaaga aagaaaaaaa ccgaacctga 100

aattcaatca gtccatagag acgaacagaa tgagaccttc cggcccaagc 1600
 gtggcgctgc gggcactttg gtagactgtg ccaccacggc gtgtgttgtg 1650
 aaacgtgaaa taaaaagagc aaaaaaaaaa 1679

<210> 523
 <211> 344
 <212> PRT
 <213> Homo sapiens

<400> 523

Met	Lys	Thr	Ile	Gln	Pro	Lys	Met	His	Asn	Ser	Ile	Ser	Trp	Ala		1	5	10	15
Ile	Phe	Thr	Gly	Leu	Ala	Ala	Leu	Cys	Leu	Phe	Gln	Gly	Val	Pro		20	25	30	
Val	Arg	Ser	Gly	Asp	Ala	Thr	Phe	Pro	Lys	Ala	Met	Asp	Asn	Val		35	40	45	
Thr	Val	Arg	Gln	Gly	Glu	Ser	Ala	Thr	Leu	Arg	Cys	Thr	Ile	Asp		50	55	60	
Asn	Arg	Val	Thr	Arg	Val	Ala	Trp	Leu	Asn	Arg	Ser	Thr	Ile	Leu		65	70	75	
Tyr	Ala	Gly	Asn	Asp	Lys	Trp	Cys	Leu	Asp	Pro	Arg	Val	Val	Leu		80	85	90	
Leu	Ser	Asn	Thr	Gln	Thr	Gln	Tyr	Ser	Ile	Glu	Ile	Gln	Asn	Val		95	100	105	
Asp	Val	Tyr	Asp	Glu	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr	Asp		110	115	120	
Asn	His	Pro	Lys	Thr	Ser	Arg	Val	His	Leu	Ile	Val	Gln	Val	Ser		125	130	135	
Pro	Lys	Ile	Val	Glu	Ile	Ser	Ser	Asp	Ile	Ser	Ile	Asn	Glu	Gly		140	145	150	
Asn	Asn	Ile	Ser	Leu	Thr	Cys	Ile	Ala	Thr	Gly	Arg	Pro	Glu	Pro		155	160	165	
Thr	Val	Thr	Trp	Arg	His	Ile	Ser	Pro	Lys	Ala	Val	Gly	Phe	Val		170	175	180	
Ser	Glu	Asp	Glu	Tyr	Leu	Glu	Ile	Gln	Gly	Ile	Thr	Arg	Glu	Gln		185	190	195	
Ser	Gly	Asp	Tyr	Glu	Cys	Ser	Ala	Ser	Asn	Asp	Val	Ala	Ala	Pro		200	205	210	
Val	Val	Arg	Arg	Val	Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	Tyr	Ile		215	220	225	
Ser	Glu	Ala	Lys	Gly	Thr	Gly	Val	Pro	Val	Gly	Gln	Lys	Gly	Thr					

	230		235		240
Leu Gln Cys Glu	Ala Ser Ala Val Pro	Ser Ala Glu Phe Gln Trp			
	245	250	255		
Tyr Lys Asp Asp	Lys Arg Leu Ile Glu	Gly Lys Lys Gly Val Lys			
	260	265	270		
Val Glu Asn Arg	Pro Phe Leu Ser Lys	Leu Ile Phe Phe Asn Val			
	275	280	285		
Ser Glu His Asp	Tyr Gly Asn Tyr Thr	Cys Val Ala Ser Asn Lys			
	290	295	300		
Leu Gly His Thr	Asn Ala Ser Ile Met	Leu Phe Gly Pro Gly Ala			
	305	310	315		
Val Ser Glu Val	Ser Asn Gly Thr Ser	Arg Arg Ala Gly Cys Val			
	320	325	330		
Trp Leu Leu Pro	Leu Leu Val Leu His	Leu Leu Leu Lys Phe			
	335	340			

<210> 524

<211> 503

<212> DNA

<213> Homo sapiens

<400> 524

gaaaaaaat catgaaaacc atccagccaa aaatgcacaa ttctatctct 50

tgggcaatct tcacggggct ggctgctctg tgtctcttcc aaggagtgcc 100

cgtgogcagc ggagatgcc ccttcccaa agctatggac aacgtgacgg 150

tccggcaggg ggagagcgcc accctcaggt gcactattga caaccggggtc 200

acccgggtgg cctgggctaaa ccgcagcacc atcctctatg ctgggaatga 250

caagtgggtgc ctggatcctc gcgtggctct tctgagcaac acccaaacgc 300

agtacagcat cgagatccag aacgtggatg tgtatgacga gggcccttac 350

acctgctcgg tgcagacaga caaccacca aagacctcta gggccacct 400

cattgtgcaa gtatctccca aaattgtaga gatttcttca gatatctcca 450

ttaatgaagg gaacaatatt agcctcacct gcatagcaac tggtagacca 500

gag 503

<210> 525

<211> 2602

<212> DNA

<213> Homo sapiens

<400> 525

atggctgggtg acggcggggc cgggcagggg accggggccg cggccccggga 50

Glu	Leu	Val	Leu	Ala	Gly	Ala	Ser	Leu	Leu	Leu	Ala	Ala	Leu	Leu		35	40	45
Leu	Gly	Cys	Leu	Val	Ala	Leu	Gly	Val	Gln	Tyr	His	Arg	Asp	Pro		50	55	60
Ser	His	Ser	Thr	Cys	Leu	Thr	Glu	Ala	Cys	Ile	Arg	Val	Ala	Gly		65	70	75
Lys	Ile	Leu	Glu	Ser	Leu	Asp	Arg	Gly	Val	Ser	Pro	Cys	Glu	Asp		80	85	90
Phe	Tyr	Gln	Phe	Ser	Cys	Gly	Gly	Trp	Ile	Arg	Arg	Asn	Pro	Leu		95	100	105
Pro	Asp	Gly	Arg	Ser	Arg	Trp	Asn	Thr	Phe	Asn	Ser	Leu	Trp	Asp		110	115	120
Gln	Asn	Gln	Ala	Ile	Leu	Lys	His	Leu	Leu	Glu	Asn	Thr	Thr	Phe		125	130	135
Asn	Ser	Ser	Ser	Glu	Ala	Glu	Gln	Lys	Thr	Gln	Arg	Phe	Tyr	Leu		140	145	150
Ser	Cys	Leu	Gln	Val	Glu	Arg	Ile	Glu	Glu	Leu	Gly	Ala	Gln	Pro		155	160	165
Leu	Arg	Asp	Leu	Ile	Glu	Lys	Ile	Gly	Gly	Trp	Asn	Ile	Thr	Gly		170	175	180
Pro	Trp	Asp	Gln	Asp	Asn	Phe	Met	Glu	Val	Leu	Lys	Ala	Val	Ala		185	190	195
Gly	Thr	Tyr	Arg	Ala	Thr	Pro	Phe	Phe	Thr	Val	Tyr	Ile	Ser	Ala		200	205	210
Asp	Ser	Lys	Ser	Ser	Asn	Ser	Asn	Val	Ile	Gln	Val	Asp	Gln	Ser		215	220	225
Gly	Leu	Phe	Leu	Pro	Ser	Arg	Asp	Tyr	Tyr	Leu	Asn	Arg	Thr	Ala		230	235	240
Asn	Glu	Lys	Val	Leu	Thr	Ala	Tyr	Leu	Asp	Tyr	Met	Glu	Glu	Leu		245	250	255
Gly	Met	Leu	Leu	Gly	Gly	Arg	Pro	Thr	Ser	Thr	Arg	Glu	Gln	Met		260	265	270
Gln	Gln	Val	Leu	Glu	Leu	Glu	Ile	Gln	Leu	Ala	Asn	Ile	Thr	Val		275	280	285
Pro	Gln	Asp	Gln	Arg	Arg	Asp	Glu	Glu	Lys	Ile	Tyr	His	Lys	Met		290	295	300
Ser	Ile	Ser	Glu	Leu	Gln	Ala	Leu	Ala	Pro	Ser	Met	Asp	Trp	Leu		305	310	315
Glu	Phe	Leu	Ser	Phe	Leu	Leu	Ser	Pro	Leu	Glu	Leu	Ser	Asp	Ser				

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320	325	330
Glu Pro Val Val Val Tyr Gly Met Asp	Tyr Leu Gln Gln Val Ser	
335	340	345
Glu Leu Ile Asn Arg Thr Glu Pro Ser	Ile Leu Asn Asn Tyr Leu	
350	355	360
Ile Trp Asn Leu Val Gln Lys Thr Thr	Ser Ser Leu Asp Arg Arg	
365	370	375
Phe Glu Ser Ala Gln Glu Lys Leu Leu	Glu Thr Leu Tyr Gly Thr	
380	385	390
Lys Lys Ser Cys Val Pro Arg Trp Gln	Thr Cys Ile Ser Asn Thr	
395	400	405
Asp Asp Ala Leu Gly Phe Ala Leu Gly	Ser Leu Phe Val Lys Ala	
410	415	420
Thr Phe Asp Arg Gln Ser Lys Glu Ile	Ala Glu Gly Met Ile Ser	
425	430	435
Glu Ile Arg Thr Ala Phe Glu Glu Ala	Leu Gly Gln Leu Val Trp	
440	445	450
Met Asp Glu Lys Thr Arg Gln Ala Ala	Lys Glu Lys Ala Asp Ala	
455	460	465
Ile Tyr Asp Met Ile Gly Phe Pro Asp	Phe Ile Leu Glu Pro Lys	
470	475	480
Glu Leu Asp Asp Val Tyr Asp Gly Tyr	Glu Ile Ser Glu Asp Ser	
485	490	495
Phe Phe Gln Asn Met Leu Asn Leu Tyr	Asn Phe Ser Ala Lys Val	
500	505	510
Met Ala Asp Gln Leu Arg Lys Pro Pro	Ser Arg Asp Gln Trp Ser	
515	520	525
Met Thr Pro Gln Thr Val Asn Ala Tyr	Tyr Leu Pro Thr Lys Asn	
530	535	540
Glu Ile Val Phe Pro Ala Gly Ile Leu	Gln Ala Pro Phe Tyr Ala	
545	550	555
Arg Asn His Pro Lys Ala Leu Asn Phe	Gly Gly Ile Gly Val Val	
560	565	570
Met Gly His Glu Leu Thr His Ala Phe	Asp Asp Gln Gly Arg Glu	
575	580	585
Tyr Asp Lys Glu Gly Asn Leu Arg Pro	Trp Trp Gln Asn Glu Ser	
590	595	600
Leu Ala Ala Phe Arg Asn His Thr Ala	Cys Met Glu Glu Gln Tyr	
605	610	615

Asn	Gln	Tyr	Gln	Val	Asn	Gly	Glu	Arg	Leu	Asn	Gly	Arg	Gln	Thr
				620					625					630
Leu	Gly	Glu	Asn	Ile	Thr	Asp	Asn	Gly	Gly	Leu	Lys	Ala	Ala	Tyr
				635					640					645
Asn	Ala	Tyr	Lys	Ala	Trp	Leu	Arg	Lys	His	Gly	Glu	Glu	Gln	Gln
				650					655					660
Leu	Pro	Ala	Val	Gly	Leu	Thr	Asn	His	Gln	Leu	Phe	Phe	Val	Gly
				665					670					675
Phe	Ala	Gln	Val	Trp	Cys	Ser	Val	Arg	Thr	Pro	Glu	Ser	Ser	His
				680					685					690
Glu	Gly	Leu	Val	Thr	Asp	Pro	His	Ser	Pro	Ala	Arg	Phe	Arg	Val
				695					700					705
Leu	Gly	Thr	Leu	Ser	Asn	Ser	Arg	Asp	Phe	Leu	Arg	His	Phe	Gly
				710					715					720
Cys	Pro	Val	Gly	Ser	Pro	Met	Asn	Pro	Gly	Gln	Leu	Cys	Glu	Val
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Trp

<210> 527

<211> 4308

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1478, 3978, 4057-4058, 4070

<223> unknown base

<400> 527

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cggctcccgg cgggcccggc gcgccggccc agagcccccc gtgctgcca 200

tccgttctga gaaggagccg ctgcccgttc ggggagcggc aggtaggtgg 250

gcgcccgggg gaggcgcggg cggggagtcg ggctcggggc ggtcagcgc 300

cagcccggag ggggcgcggg gcgcaggtgg ctcggcgcgg cgggcggccc 350

ggaggggtgg cgggggcaga agggcgcggt gcctgggacc cgggacccgc 400

gggcagcccc cggggcggca cacggcgcga gctgggcagc ggcctccagc 450

caagcccgtc ccgcaggct gcaccttcgg cgggaaggtc tatgccttgg 500

gcctctccac tccctctccc ctctccaac attccctccc ttctgtctcc 3450
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<210> 528

<211> 1285

<212> DNA

<213> Homo sapiens

<400> 528

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 ccctgaatca ccgcctggcc cgactccacc atgaacgtcg cgctgcagga 150
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 taggctcacg cacgcagctg gagctggtct tagcaggtgc ctctctactg 250
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 gctgagcaga agacacagcg cttctaccta tcttgccctac aggtggagcg 600
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 gtggttggaa cattaogggg ccctgggacc aggacaactt tatggagggtg 700
 ttgaaggcag tagcagggac ctacagggcc accccattct tcaccgtcta 750
 catcagtgcc gactctaaga gttccaacag caatgttatc caggtggacc 800
 agtctgggct ctttctgccc tctcgggatt actacttaaa cagaactgcc 850
 aatgagaaag taaggaacat cttccgaacc cccatcccta ccctggctg 900
 agctgggctg atccctgttg acttttccct ttgccaaggg tcagagcagg 950
 gaaggtgagc ctatcctgtc acctagttaa caaactgccc ctcccttctt 1000
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 ttctcttat tcttctagta ggtttcatag acacctactg tgtgccaggt 1100
 ccagtggggg aattcggaga tataagtttc cgagccattg ccacaggaag 1150
 cgttcagtgt cgatgggttc atggacctag ataggctgat aacaaagctc 1200
 acaagagggg cctgaggatt caggagagac ttatggagcc agcaaagtct 1250
 tcctgaagag attgcatttg agccaggtcc tgtag 1285

<210> 529
 <211> 1380
 <212> DNA
 <213> Homo sapiens

<400> 529
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 ctgcaggccc ctttctatgc ccgcaaccac cccaaggccc tgaacttcgg 100
 tggcatcggt gtggtcatgg gccatgagtt gacgcatgcc tttgatgacc 150
 aagggcgcgga gtatgacaaa gaagggaacc tgcggccctg gtggcagaat 200
 gagtccctgg cagccttccg gaaccacacg gcctgcatgg aggaacagta 250
 caatcaatac caggtcaatg gggagaggct caacggccgc cagacgctgg 300
 gggagaacat tgctgacaac ggggggctga aggtgccta caatgcttac 350

aaagcatggc	tgagaaaagca	tggggaggag	cagcaactgc	cagccgtggg	400
gctcaccaac	caccagctct	tcttcgtggg	atttgcccag	gtgtggtgct	450
cggtccgcac	accagagagc	tctcacgagg	ggctggtgac	cgacccccac	500
agccctgccc	gcttccgcgt	gctgggcact	ctctccaact	cccgtgactt	550
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cagacctggg	gcagctctcc	tgacaaagct	gtttgctctt	gggttgggag	700
gaagcaaagt	caagctgggc	tgggtctagt	ccctcccccc	cacaggtgac	750
atgagtacag	accctcctca	atcaccacat	tgtgcctctg	ctttgggggt	800
gcccctgcct	ccagcagagc	cccaccatt	cactgtgaca	tctttccgtg	850
tcaccctgcc	tggaagaggt	ctgggtgggg	aggccagttc	ccataggaag	900
gagtctgcct	cttctgtccc	caggctcact	cagcctggcg	gccatggggc	950
ctgccgtgcc	tgccccactg	tgaccacag	gcctgggtgg	tgtacctcct	1000
ggactttctc	ccaggctcac	tcagtgcgca	cttaggggtg	gactcagctc	1050
tgtctggctc	accctcacgg	gctaccccc	cctcaccctg	tgtccttgt	1100
gccactgctc	ccagtgtgc	tgctgacctt	cactgacagc	tcctagtggg	1150
agcccaaggg	cctctgaaag	cctcctgctg	cccactgttt	ccctgggctg	1200
agaggggaag	tgcatatgtg	tagcgggtac	tggttcctgt	gtcttagggc	1250
acaagcctta	gcaaatgatt	gattctccct	ggacaaagca	ggaaagcaga	1300
tagagcaggg	aaaaggaaga	acagagttta	tttttacaga	aaagaggggtg	1350
ggaggggtgtg	gtcttgcccc	ttataggacc	1380		

<210> 530

<211> 39

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic oligonucleotide probe

<400> 530

gaagcagtgc agccagcagt agagagggcac ctgctaaga 39

<210> 531

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 531
acgcagctgg agctggtctt agca 24

<210> 532
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 532
ggtactggac ccctagggcc acaa 24

<210> 533
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 533
cctcccagcc gagaccagtg g 21

<210> 534
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 534
ggtoctataa gggccaagac c 21

<210> 535
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
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<400> 535
gactagttct agatcgcgag cggccgccct tttttttttt tttt 44

<210> 536
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 536
cggacgcgtg ggtcga 16

<210> 537
<211> 21
<212> DNA
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<220>
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<400> 537
cggccgtgat ggctggtgac g 21

<210> 538
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<212> DNA
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<220>
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ggcagactcc ttcctatggg 20

<210> 539
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<212> DNA
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ggcacttcat ggtccttgaa a 21

<210> 540
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<220>
<223> Synthetic oligonucleotide probe

<400> 540
cggatgtgtg tgaggccatg cc 22

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<212> DNA
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<400> 541
gaaagtaacc acggaggtca agat 24

<210> 542
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cctcctccga gactgaaagc t 21

<210> 543
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<400> 543
tcgcgttgct ttttctcgcg tg 22

<210> 544
<211> 17
<212> DNA
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<220>
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<400> 544
gcgtgcgtca ggttcca 17

<210> 545
<211> 19
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 545
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Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala	50	55	60
Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	65	70	75
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	80	85	90
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	95	100	105
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu	110	115	120
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	125	130	135
Asn	Phe	Thr	Gln	Asn	Pro	Gly	Met	Phe	Arg	Ile	Lys	Gly	Glu	Gln	140	145	150
Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro	155	160	165
Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Glu	Lys	Gly	Ala	Lys	170	175	180
Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln	185	190	195
Gly	Pro	Pro	Gly	Val	Lys	Gly	Glu	Ala	Gly	Leu	Gln	Gly	Pro	Gln	200	205	210
Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln	215	220	225
Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys	230	235	240
Gly	Glu	Thr	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Asp	Leu	Gly	Leu	Pro	245	250	255
Gly	Ser	Lys	Gly	Asp	Arg	Gly	Met	Lys	Gly	Asp	Ala	Gly	Val	Met	260	265	270
Gly	Pro	Pro	Gly	Ala	Gln	Gly	Ser	Lys	Gly	Asp	Phe	Gly	Arg	Pro	275	280	285
Gly	Pro	Pro	Gly	Leu	Ala	Gly	Phe	Pro	Gly	Ala	Lys	Gly	Asp	Gln	290	295	300
Gly	Gln	Pro	Gly	Leu	Gln	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val	305	310	315
Gly	His	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Ser	Pro			

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 gatgtgagat gatctgttac tgcaacttca gcgaattgct ctgctgcca 400
 aaagacgttt tctttggacc aaagatctct ttctgtattc cttgcaacaa 450
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 aaactgcaact acatcagtat aactgcattt ctagtttcta tatagtgcaa 550
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<210> 616
 <211> 98
 <212> PRT
 <213> Homo Sapien

<400> 616

Met	Lys	Leu	Met	Val	Leu	Val	Phe	Thr	Ile	Gly	Leu	Thr	Leu	Leu
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Leu	Gly	Val	Gln	Ala	Met	Pro	Ala	Asn	Arg	Leu	Ser	Cys	Tyr	Arg
			20					25						30
Lys	Ile	Leu	Lys	Asp	His	Asn	Cys	His	Asn	Leu	Pro	Glu	Gly	Val
			35					40						45
Ala	Asp	Leu	Thr	Gln	Ile	Asp	Val	Asn	Val	Gln	Asp	His	Phe	Trp
			50					55						60
Asp	Gly	Lys	Gly	Cys	Glu	Met	Ile	Cys	Tyr	Cys	Asn	Phe	Ser	Glu
			65					70						75
Leu	Leu	Cys	Cys	Pro	Lys	Asp	Val	Phe	Phe	Gly	Pro	Lys	Ile	Ser
			80					85						90
Phe	Val	Ile	Pro	Cys	Asn	Asn	Gln							
			95											

<210> 617
 <211> 2558
 <212> DNA
 <213> Homo Sapien

<400> 617

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 ggggtcccggg aggcggctc tgctcgcgc gagatgtgga atctccttca 200
 cgaaaccgac tcggctgtgg ccaccgcgc cgcggcgcgc tggctgtgcg 250
 ctggggcgct ggtgctggcg ggtggcttct ttctcctcgg cttcctcttc 300

ggggtggttta taaaatcctc caatgaagct actaacatta ctccaaagca 350
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<210> 618

<211> 750

<212> PRT

<213> Homo Sapien

<400> 618

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Arg	Arg	Pro	Arg	Trp	Leu	Cys	Ala	Gly	Ala	Leu	Val	Leu	Ala	Gly
			20					25						30
Gly	Phe	Phe	Leu	Leu	Gly	Phe	Leu	Phe	Gly	Trp	Phe	Ile	Lys	Ser
			35					40						45
Ser	Asn	Glu	Ala	Thr	Asn	Ile	Thr	Pro	Lys	His	Asn	Met	Lys	Ala
			50					55						60
Phe	Leu	Asp	Glu	Leu	Lys	Ala	Glu	Asn	Ile	Lys	Lys	Phe	Leu	His
			65					70						75
Asn	Phe	Thr	Gln	Ile	Pro	His	Leu	Ala	Gly	Thr	Glu	Gln	Asn	Phe
			80					85						90

Gln	Leu	Ala	Lys	Gln	Ile	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu	95	100	105
Asp	Ser	Val	Glu	Leu	Ala	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	110	115	120
Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly	125	130	135
Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Glu	Pro	Pro	Pro	Pro	Gly	140	145	150
Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser	155	160	165
Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala	170	175	180
Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn	185	190	195
Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg	200	205	210
Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Val	215	220	225
Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys	230	235	240
Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg	245	250	255
Gly	Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro	260	265	270
Gly	Tyr	Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu	275	280	285
Ala	Val	Gly	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	290	295	300
Asp	Ala	Gln	Lys	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	305	310	315
Asp	Ser	Ser	Trp	Arg	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	320	325	330
Pro	Gly	Phe	Thr	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	335	340	345
Ile	His	Ser	Thr	Asn	Glu	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	350	355	360
Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly	365	370	375
Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser			

	380	385	390
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr	Leu
	395	400	405
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala	Ser
	410	415	420
Trp Asp Ala Glu	Glu Phe Gly Leu Leu	Gly Ser Thr Glu Trp	Ala
	425	430	435
Glu Glu Asn Ser	Arg Leu Leu Gln Glu	Arg Gly Val Ala Tyr	Ile
	440	445	450
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val	Asp
	455	460	465
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys	Glu
	470	475	480
Leu Lys Ser Pro	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr	Glu
	485	490	495
Ser Trp Thr Lys	Lys Ser Pro Ser Pro	Glu Phe Ser Gly Met	Pro
	500	505	510
Arg Ile Ser Lys	Leu Gly Ser Gly Asn	Asp Phe Glu Val Phe	Phe
	515	520	525
Gln Arg Leu Gly	Ile Ala Ser Gly Arg	Ala Arg Tyr Thr Lys	Asn
	530	535	540
Trp Glu Thr Asn	Lys Phe Ser Gly Tyr	Pro Leu Tyr His Ser	Val
	545	550	555
Tyr Glu Thr Tyr	Glu Leu Val Glu Lys	Phe Tyr Asp Pro Met	Phe
	560	565	570
Lys Tyr His Leu	Thr Val Ala Gln Val	Arg Gly Gly Met Val	Phe
	575	580	585
Glu Leu Ala Asn	Ser Ile Val Leu Pro	Phe Asp Cys Arg Asp	Tyr
	590	595	600
Ala Val Val Leu	Arg Lys Tyr Ala Asp	Lys Ile Tyr Ser Ile	Ser
	605	610	615
Met Lys His Pro	Gln Glu Met Lys Thr	Tyr Ser Val Ser Phe	Asp
	620	625	630
Ser Leu Phe Ser	Ala Val Lys Asn Phe	Thr Glu Ile Ala Ser	Lys
	635	640	645
Phe Ser Glu Arg	Leu Gln Asp Phe Asp	Lys Ser Asn Pro Ile	Val
	650	655	660
Leu Arg Met Met	Asn Asp Gln Leu Met	Phe Leu Glu Arg Ala	Phe
	665	670	675

Ile	Asp	Pro	Leu	Gly	Leu	Pro	Asp	Arg	Pro	Phe	Tyr	Arg	His	Val
				680					685					690
Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly	Glu	Ser	Phe
				695					700					705
Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Glu	Ser	Lys	Val	Asp
				710					715					720
Pro	Ser	Lys	Ala	Trp	Gly	Glu	Val	Lys	Arg	Gln	Ile	Tyr	Val	Ala
				725					730					735
Ala	Phe	Thr	Val	Gln	Ala	Ala	Ala	Glu	Thr	Leu	Ser	Glu	Val	Ala
				740					745					750

<210> 619

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 619

agatgtgaag gtgcaggtgt gccg 24

<210> 620

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 620

gaacatcagc gctcccggta attcc 25

<210> 621

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 621

ccagcctttg aatggtacaa aggagagaag aagctcttca atggcc 46

<210> 622

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 622

ccaaactcac ccagtgagtg tgagc 25

<210> 623
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 623
tgggaaatca ggaatggtgt tctcc 25

<210> 624
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide probe

<400> 624
cttgttttca ccattgggct aactttgctg ctaggagttc aagccatgcc 50